



O A 1 2 3 4 5 - Days p.i.

 = RIDβ

 = 14.7K

 = gp19K

a b c d e f g

FIGURE 29

09141911.070998

358020-1161160

gp19K

RID β

14.7K

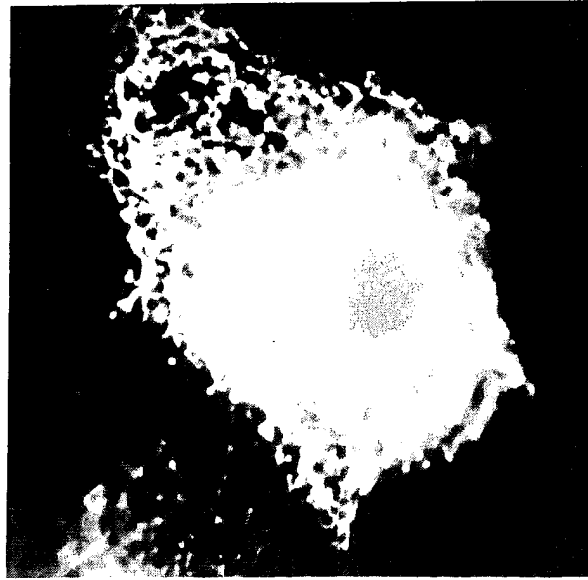


FIGURE 30A



FIGURE 30B



FIGURE 30C

TNFR1	362	V V E N V P P L R W K E F V R R L G L S D H E I D R L E L Q N G R C L R E A Q Y	401
Fas	236	I A G V M T L S Q V K G E V R K N G V N E A K L D E E I K N D N V Q D T A E Q K V	275
DR3	338	V M D A V P A R R W K E F V R T L G L R E A E I E A V E V E I G R - F R D Q Q Y	376
TRAIL-R1	348	F A N I V P F D S W D Q L M R Q L D L T K N F E I D V V R A G T A G - P G D A L Y	386
TRAIL-R2	316	F A D L V P F D S W E P L M R K E G L M D N E I K V A K A E A A G - H R D T L Y	354
TNFR1	402	S M L A T W R R R T P R R E A T L E L L G R V L R D M D L L G C L E D I E E	439
Fas	276	Q L L R N W H Q L H G K - K E A Y D T L I K D L K K A N L C T L A E K I Q T	313
DR3	377	E M L K R W R - - Q Q Q - P A G L G A V Y A A L E R M G L D G C V E D L R S	411
TRAIL-R1	387	A M L M K W V N K T G R - N A S I H T L L D A L E R M E E R H A K E K I Q D	423
TRAIL-R2	356	T M L I K W V N K T G R - D A S V H T L L D A L E T L G E R L A K Q K I E D	392

Figure 1

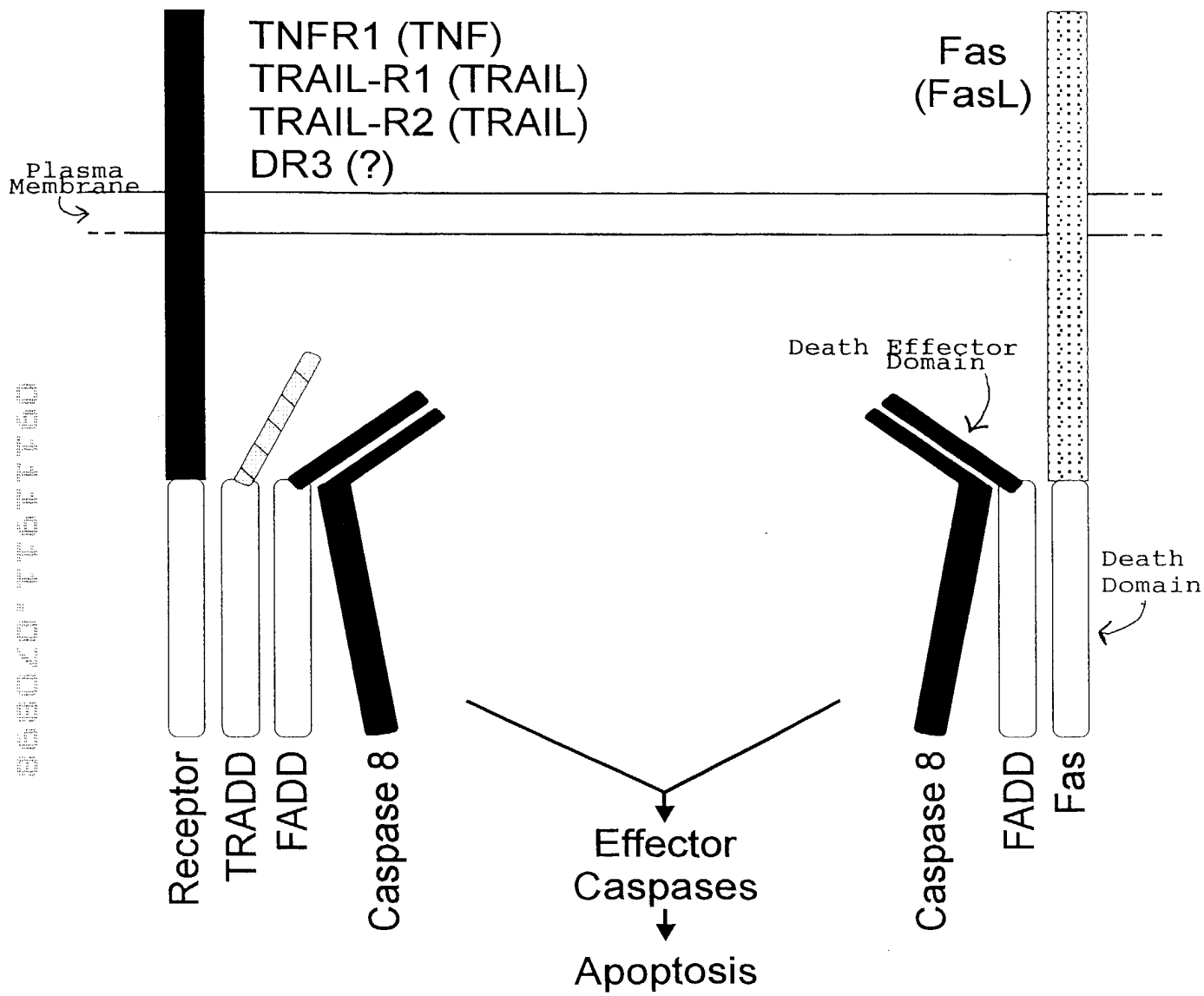


FIGURE 2

RID COMPLEX

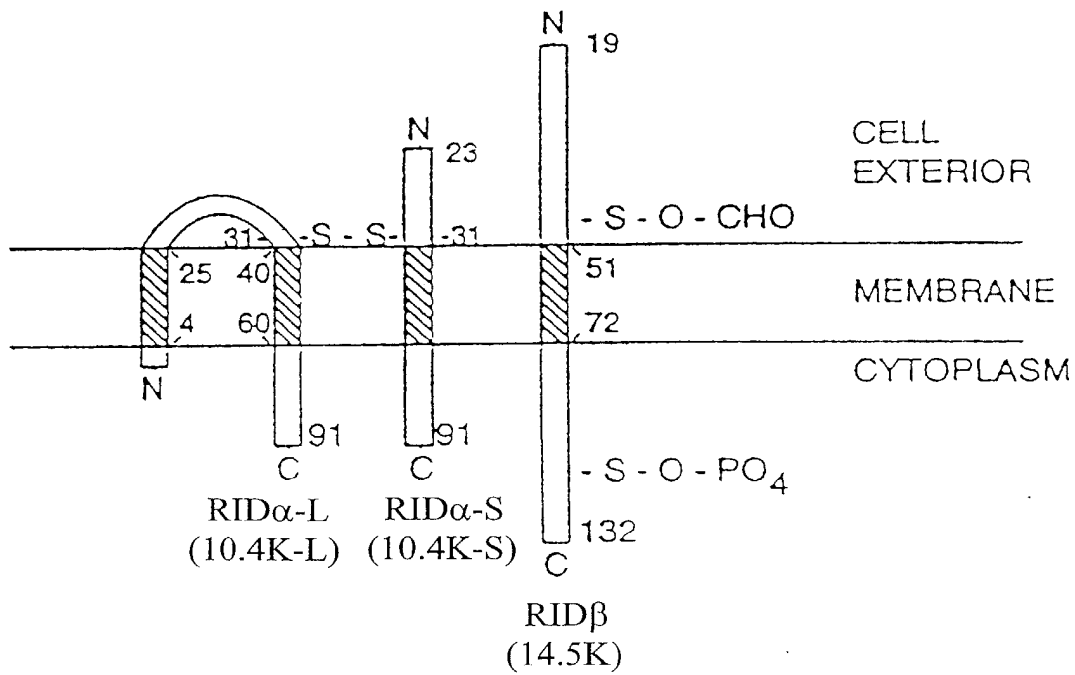


FIGURE 3

[illegible][illegible][illegible][illegible][illegible][illegible]

Pre-RID β (14.5K)

10 20
M K F T V T F L L I I C T L S A F C S P T S K P Q R H I
 signal sequence
 30 40 50
 S C R F T R I W N I P S C Y N E K S D L S E A W L Y A I
 60 70 80
I S V M V F C S T I L A L A I Y P Y L D I G W N A I D A
 Transmembrane
 90 100 110
 M N H P T F P A P A M L P L Q Q V V A G G F V P A N Q P
 120 130
 R P P S P T P T E I S Y F N L T G G D D
 * *

Figure 4C

Mature-RID β (14.5K)

10 20
 S P T S K P Q R H I S C R F T R I W N I P S C Y N E K S
 30 40 50
 D L S E A W L Y A I I S V M V F C S T I L A L A I Y P Y
 Transmembrane
 60 70 80
 L D I G W N A I D A M N H P T F P A P A M L P L Q Q V V
 90 100 110
 A G G F V P A N Q P R P P S P T P T E I S Y F N L T G G
 * *
 D D

Figure 4D



FIGURE 25



FIGURE 24

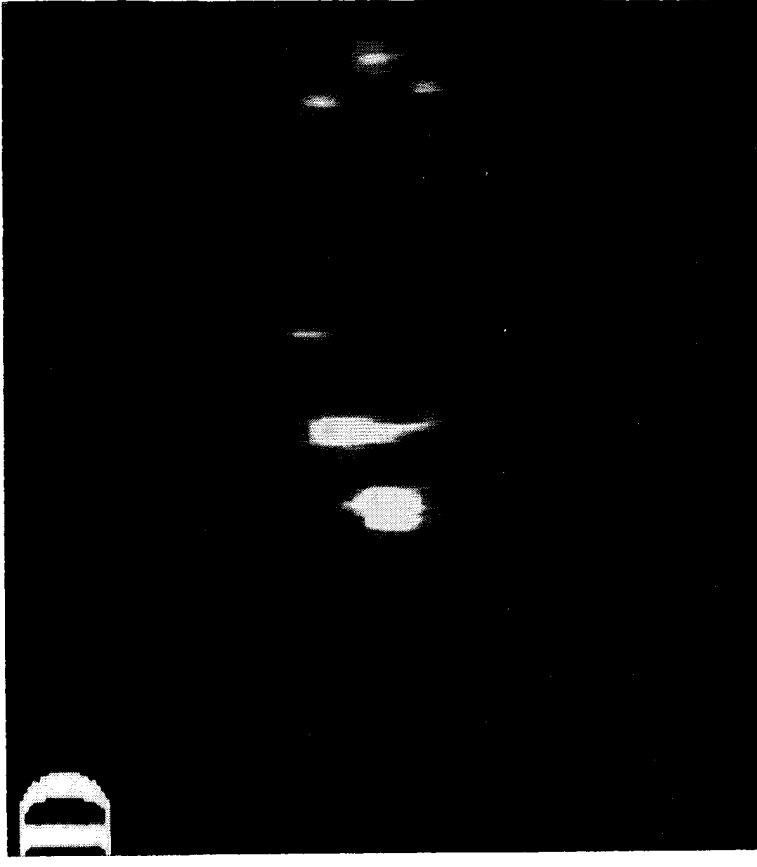
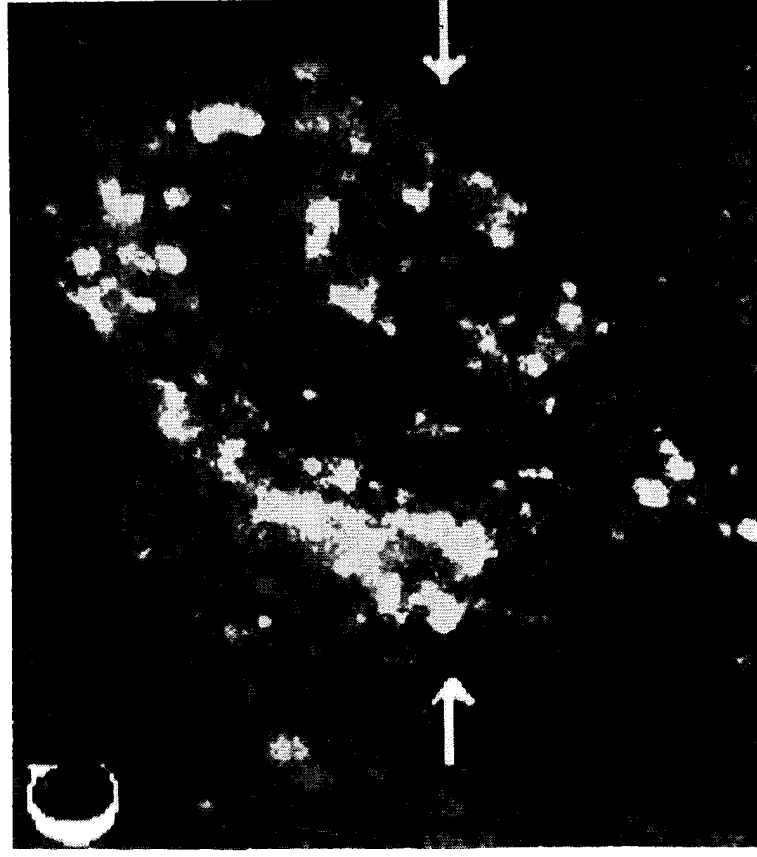
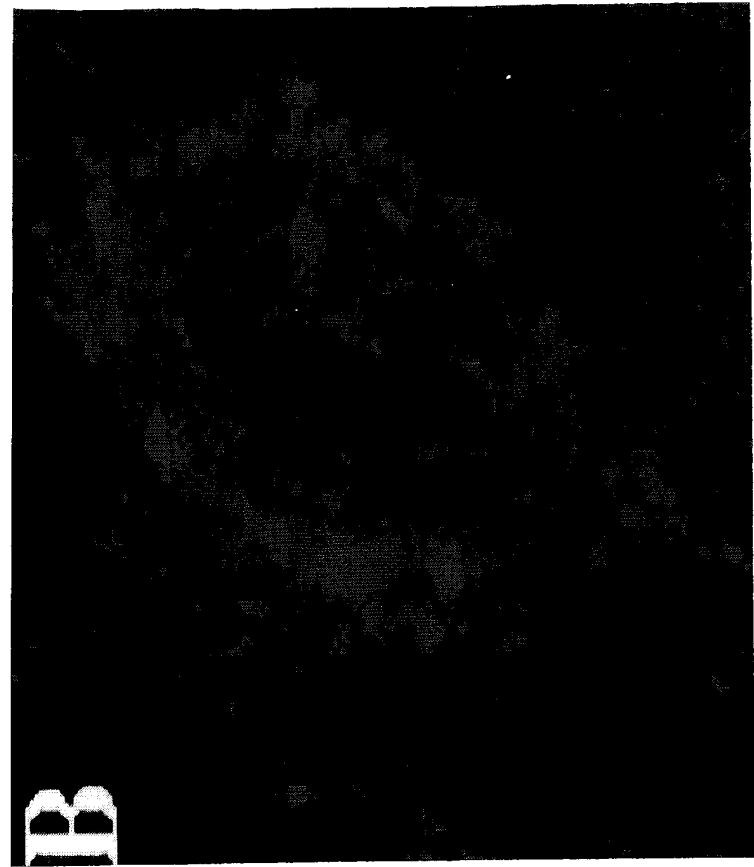
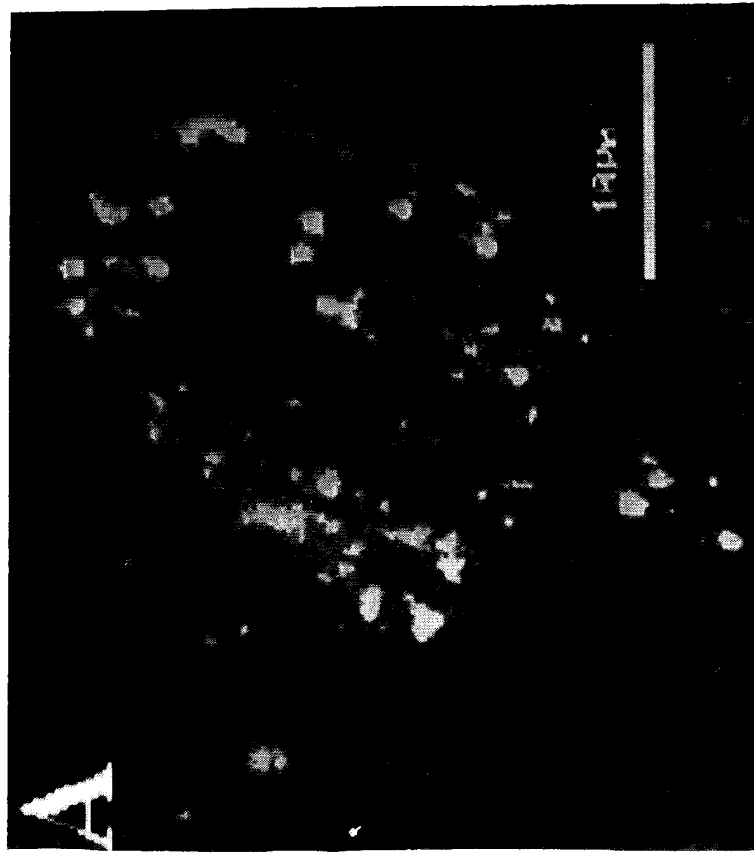


FIGURE 12

FIGURE 11

A. RID α , anti-RID α



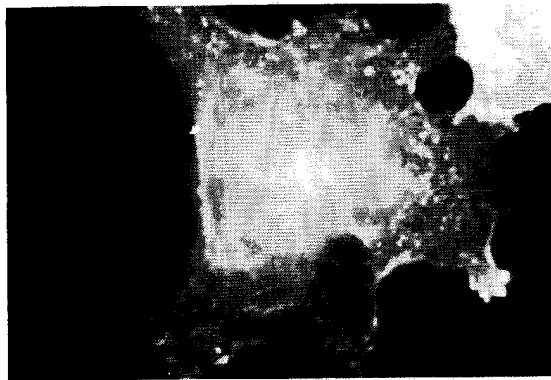
B. RID α , anti-Fas



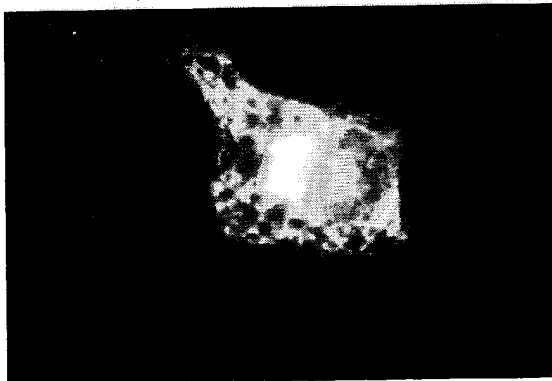
C. RID β , anti-RID β



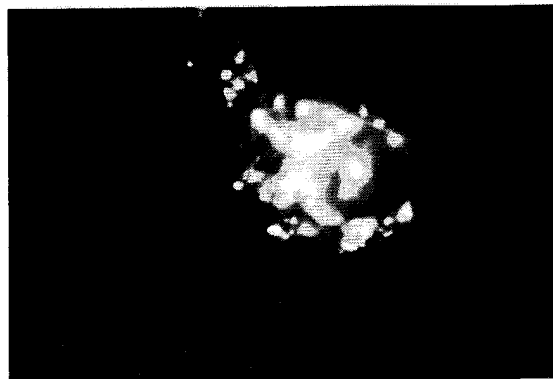
D. RID β , anti-Fas



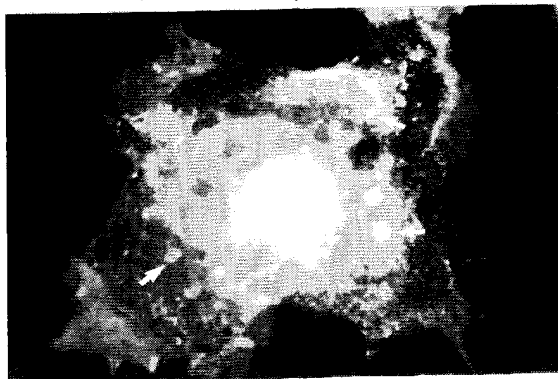
E. RID, anti-RID α



F. RID, anti-Fas



G. RID, anti-RID β



H. RID, anti-Fas



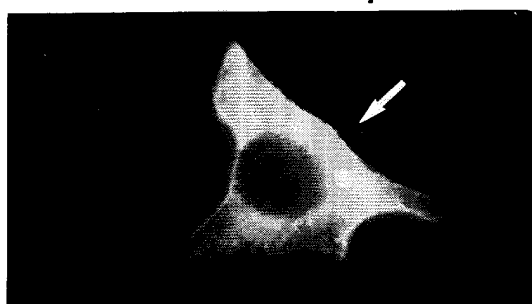
A. *rec700*, anti-DPB



B. *rec700*, DAPI



C. RID, anti-RID β



D. RID, DAPI

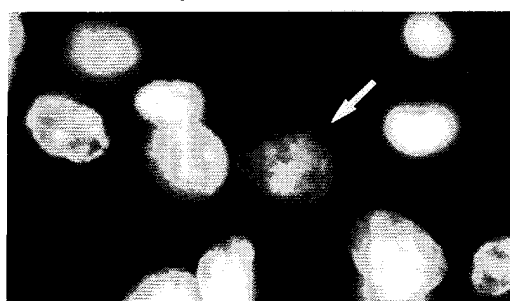
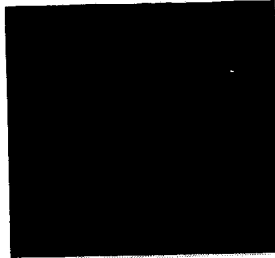


FIGURE 6

A. MCF7, Mock



B. MCF7-Fas, Mock



C. *rec700* (Wild Type)



D. *dl309* (RID⁻, 14.7K⁻)



E. *dl748* (RID α ⁻, RID β ⁺)



F. *dl764* (RID α ⁺, RID β ⁻)



G. *dl758* (RID⁺, 14.7K⁺)



H. *pm760* (RID \uparrow)

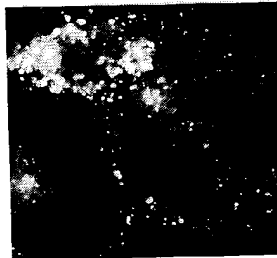


FIGURE 9

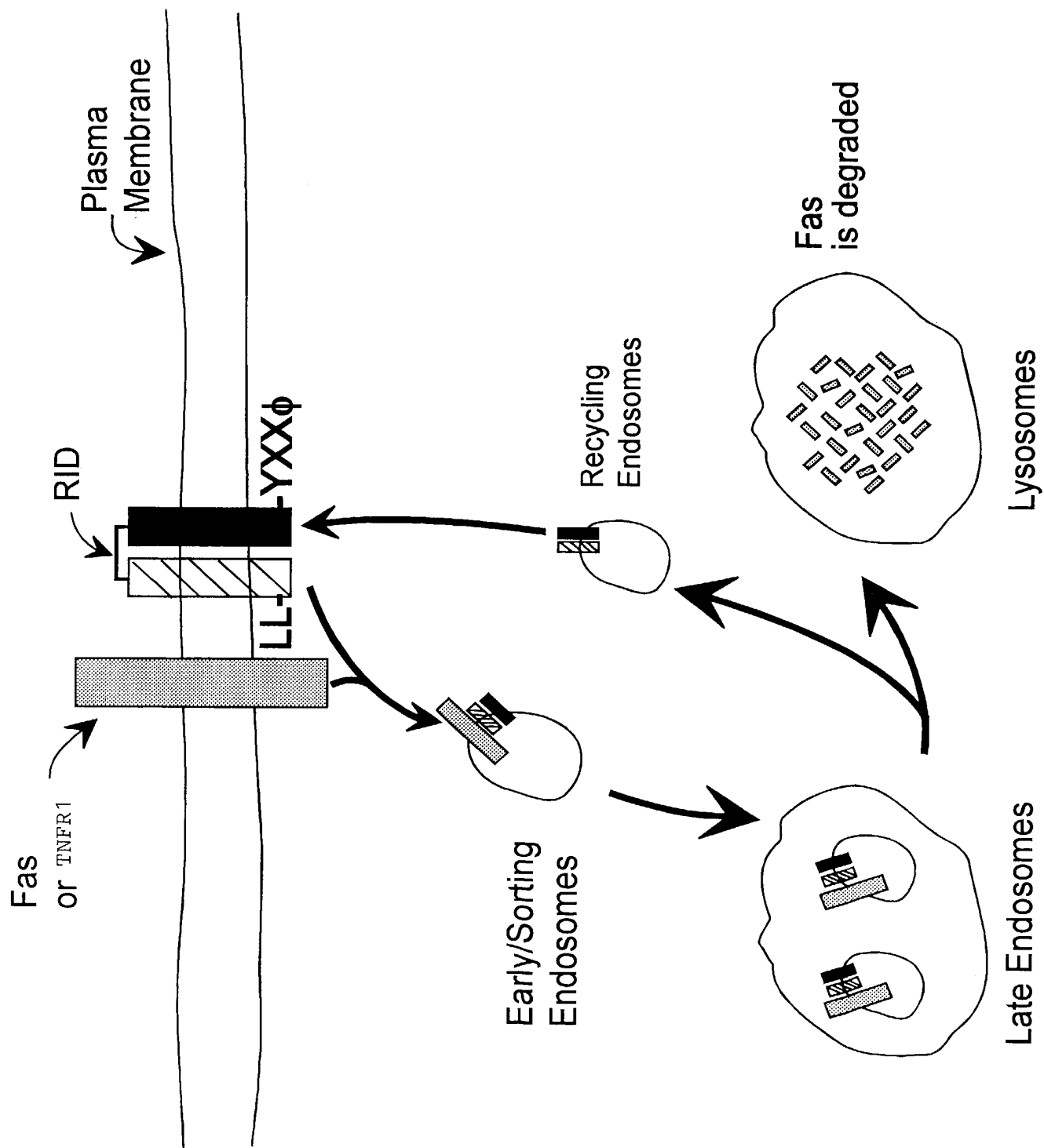


FIGURE 5

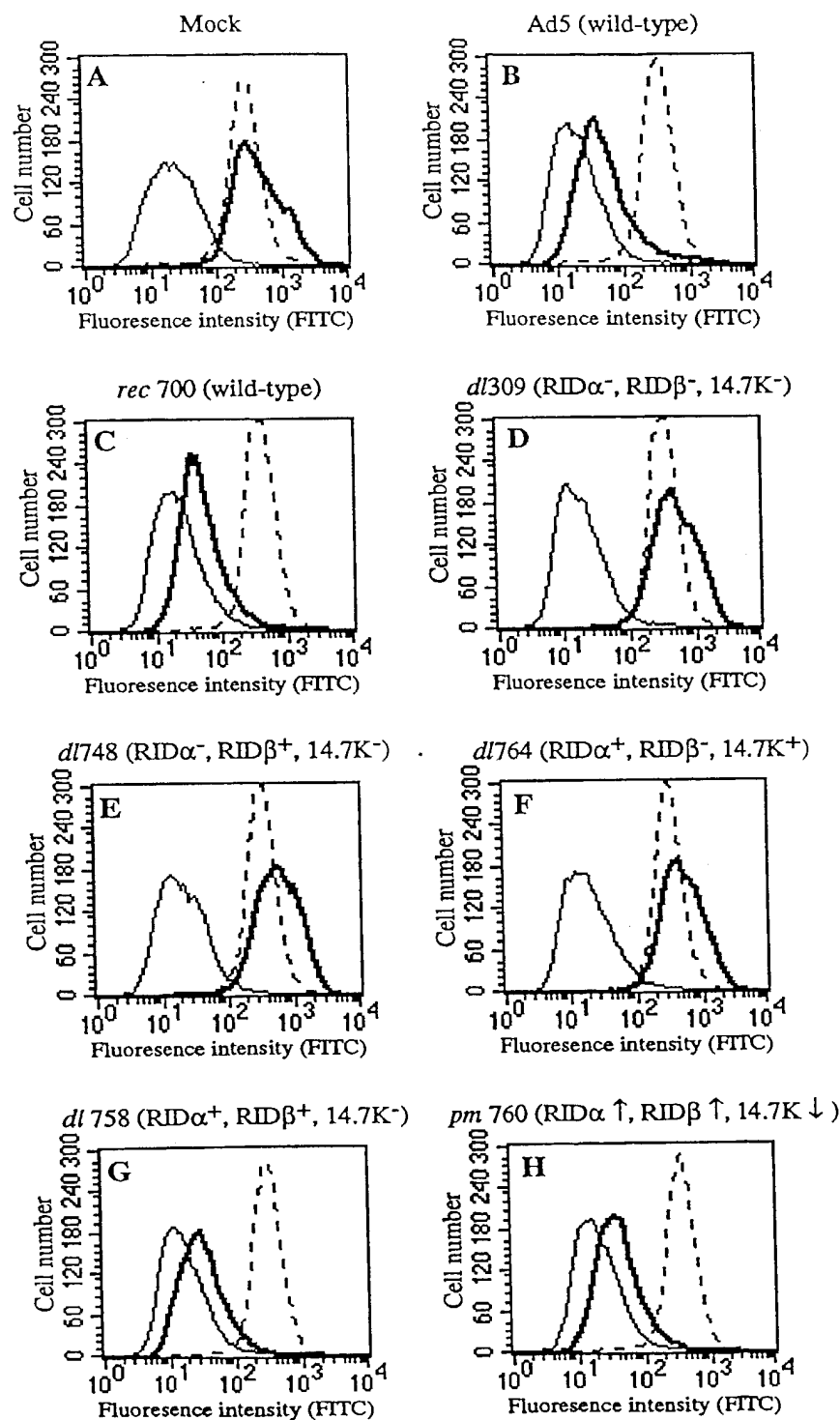


FIGURE 7

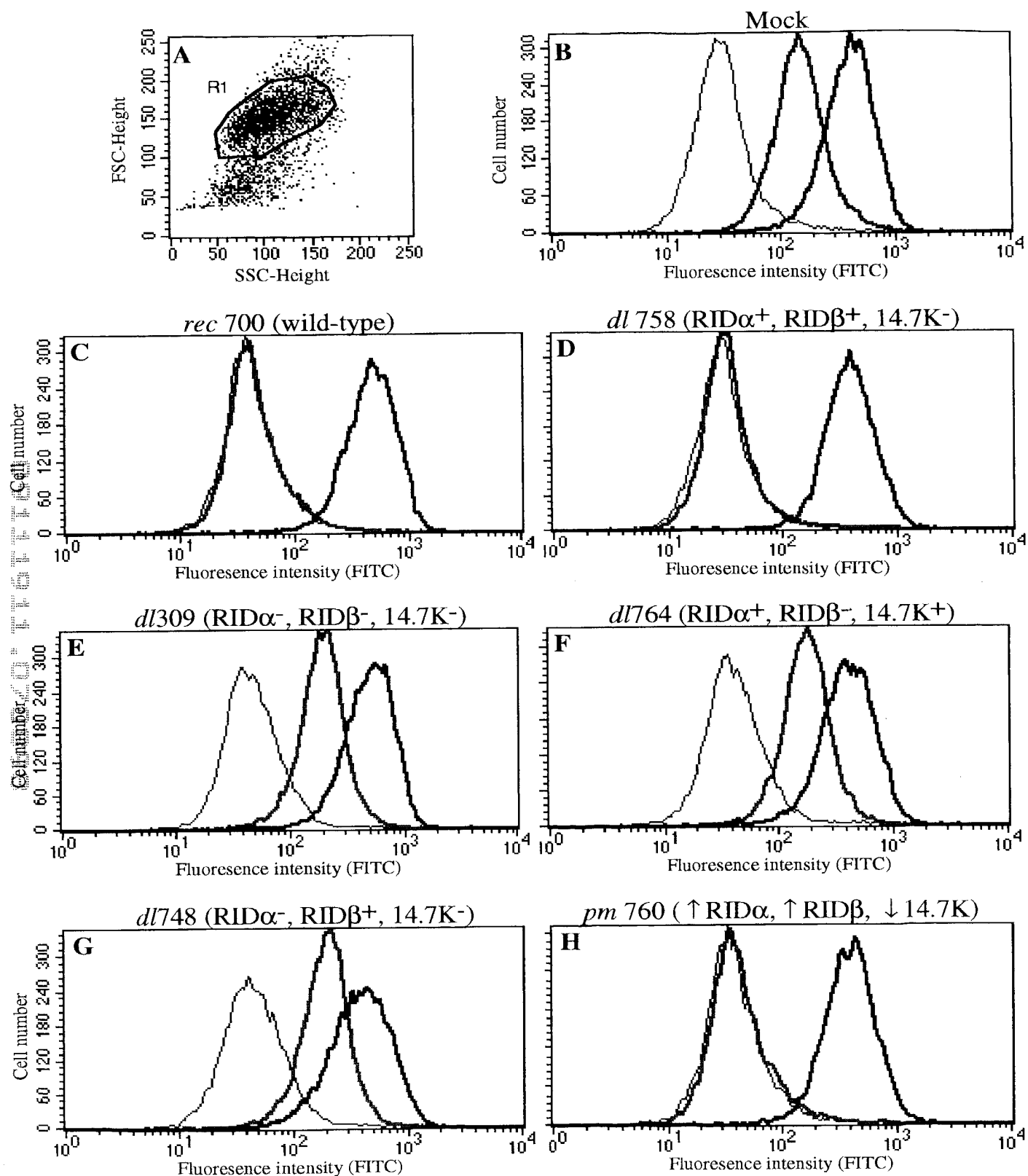


FIGURE 8

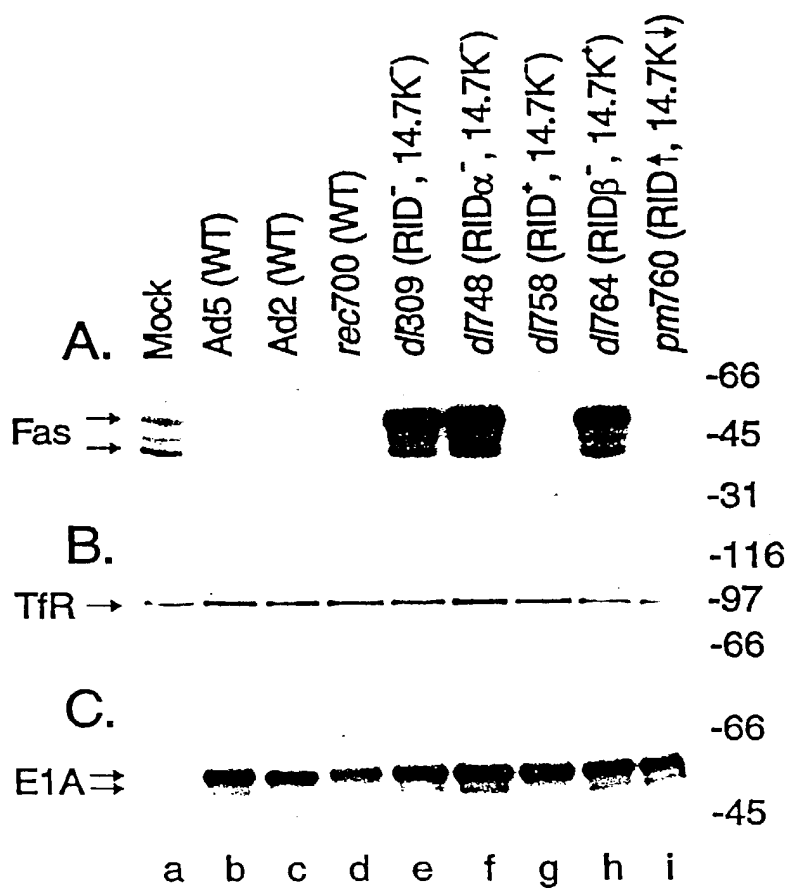
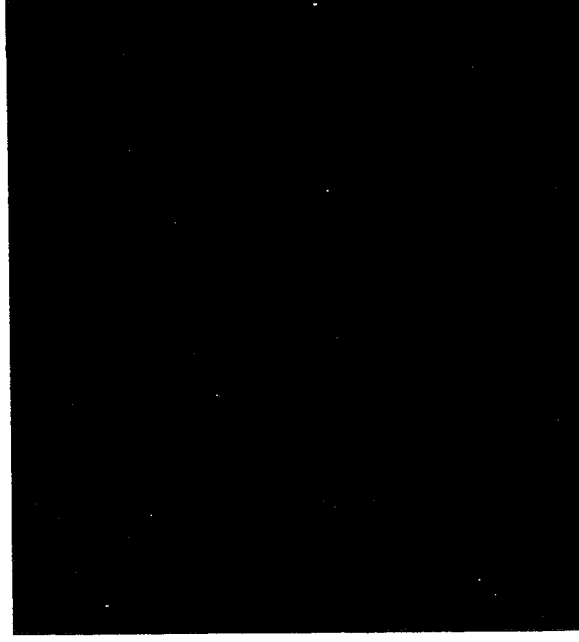
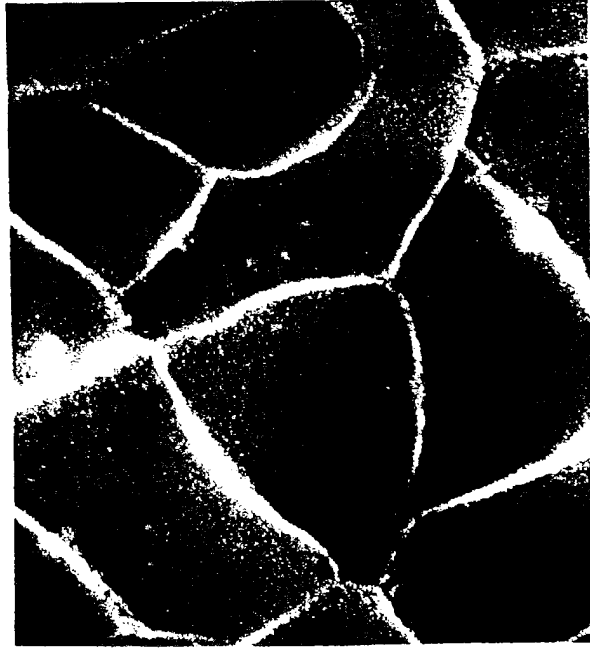


FIGURE 10

A *rec700* (WT), Baf⁺ B *rec700* (WT), Baf⁻



C *d/309* (RID⁻), Baf⁺



D Mock 700 309

Baf - + - + - +



Fas

ERp72 →

E1B-19K →

FIGURE 13 a b c d e f

	Mock		700	309	
Baf	-	+	-	+	-
TfR	— — — — —				

FIGURE 13E

0944941.070898

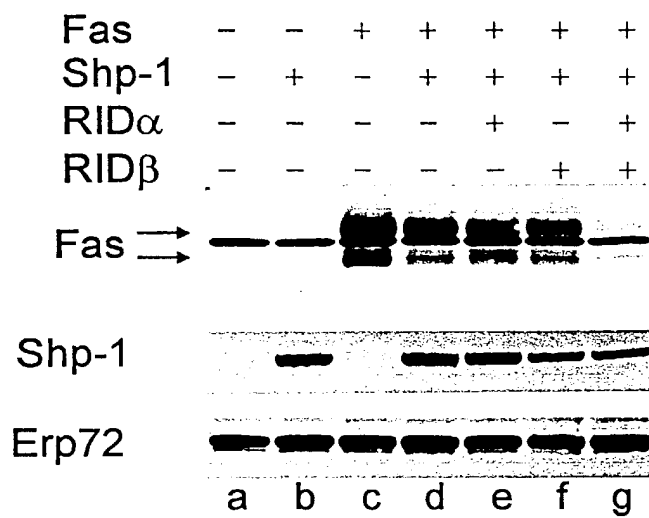


FIGURE 14

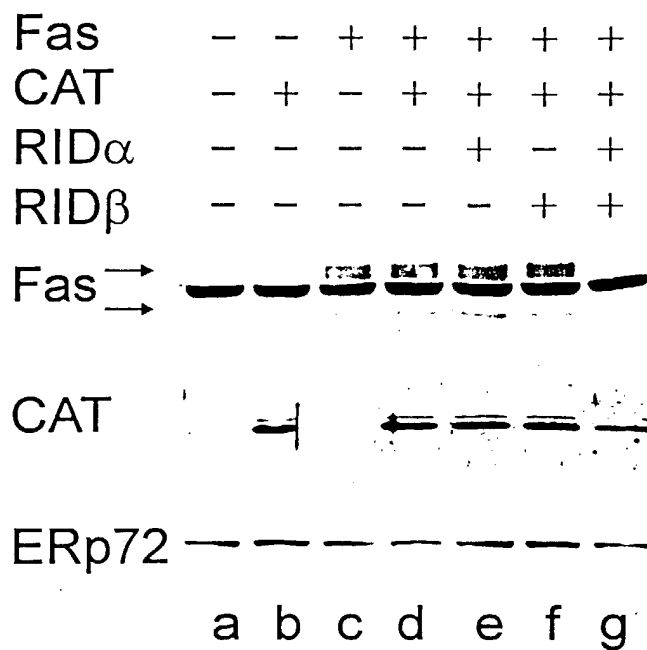


FIGURE 15

A. CTL From Perforin (-/-) Mice

Condition	% Specific Lysis
Mock	~75
<i>rec700</i> (WT)	~52
<i>d17001</i> (E3 ⁻)	~38

B. CTL From Perforin (+/+) Mice

Condition	% Specific Lysis
Mock	~75
<i>rec700</i> (WT)	~48
<i>d17001</i> (E3 ⁻)	~52

C. FACS in Infected P815 Cells

FL2-Counts

Counts

10⁰ 10¹ 10² 10³ 10⁴

FL2-Counts

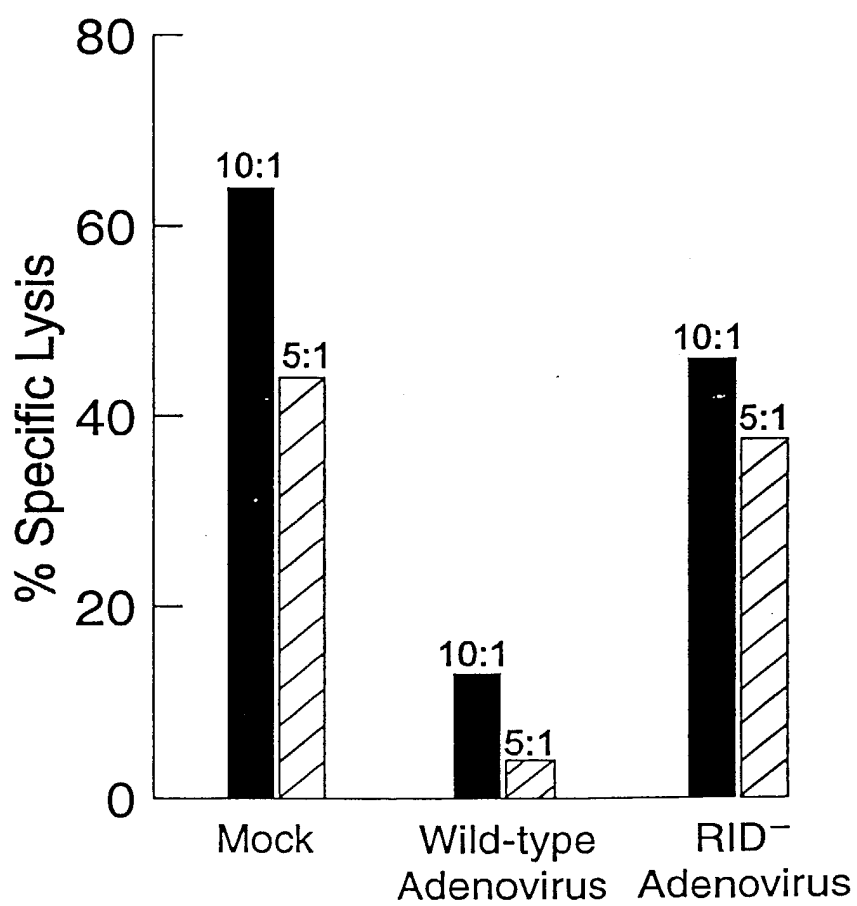


FIGURE 17

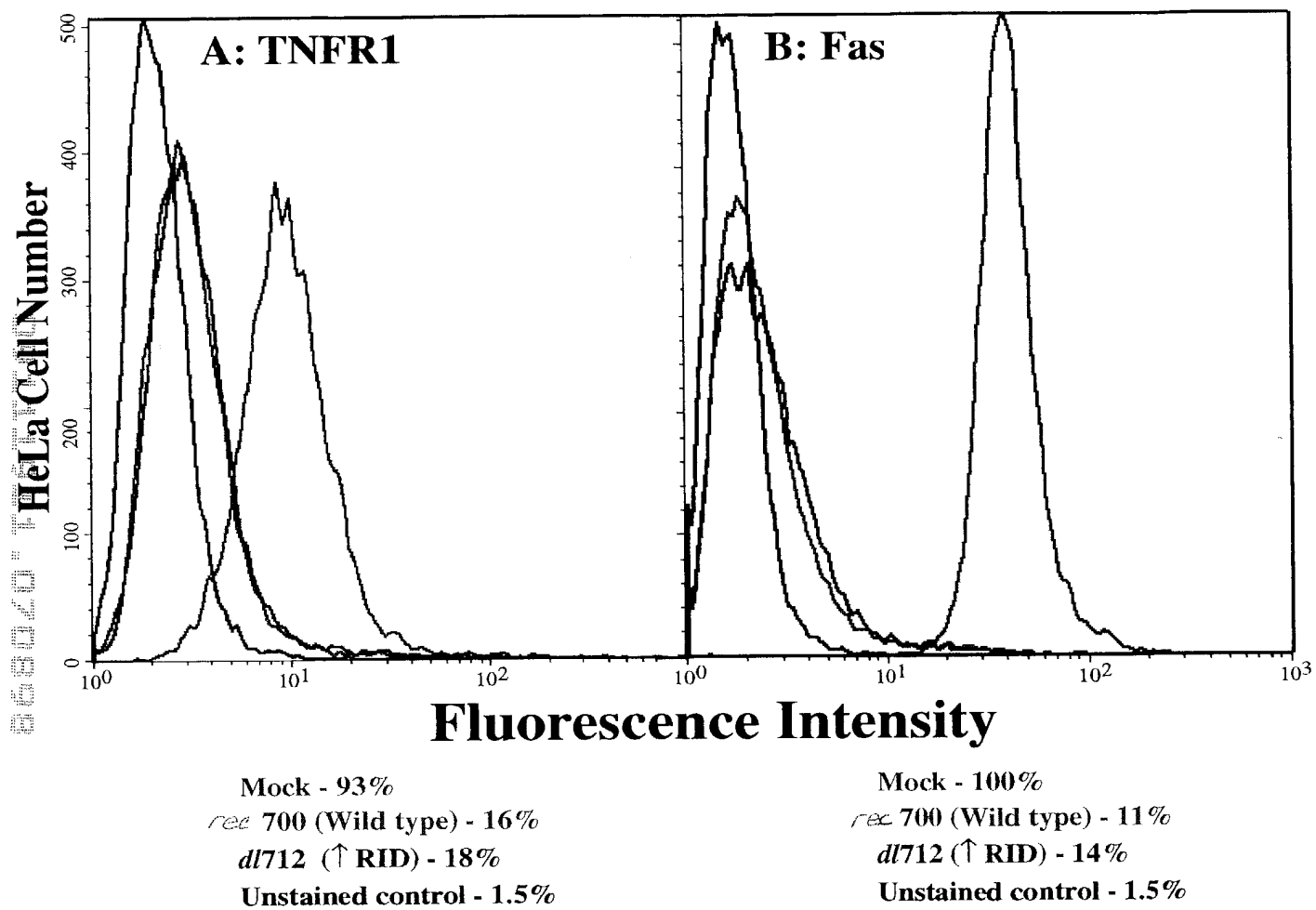


FIGURE 18

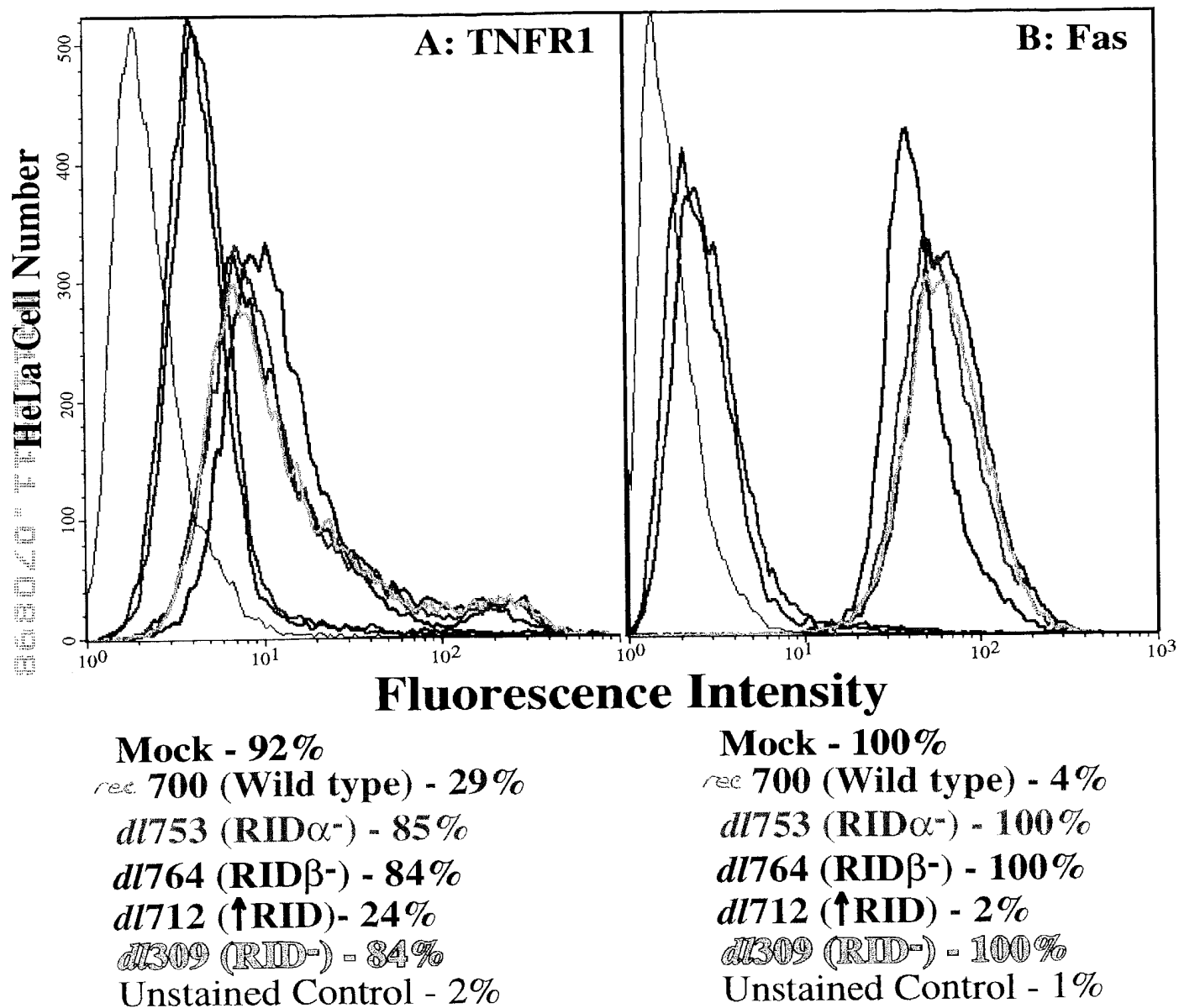
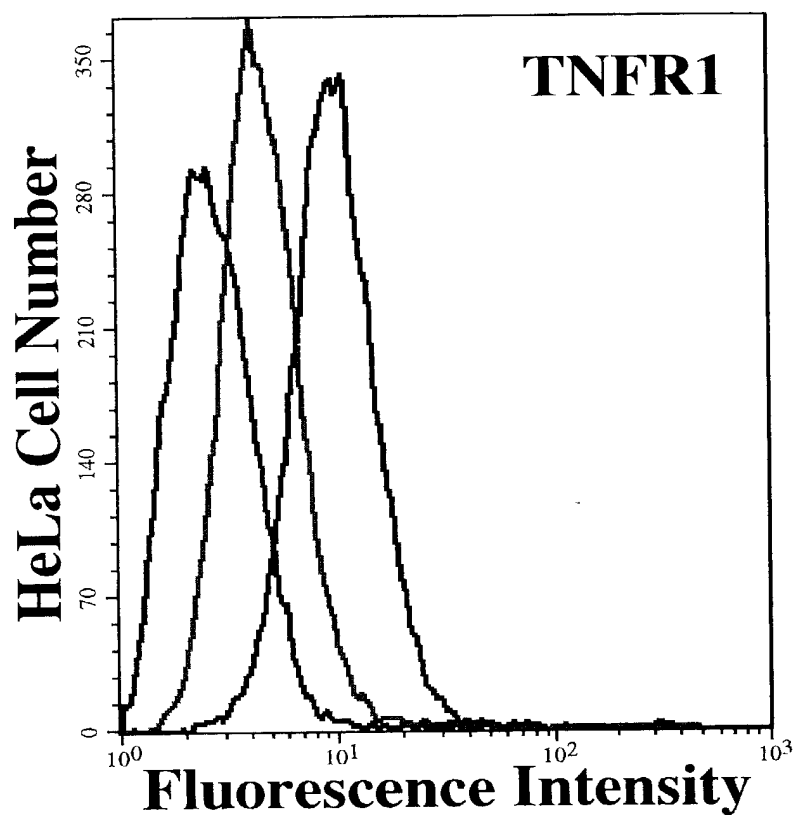


FIGURE 19



Mock - 93%

231-10 (E3⁺ vector) 24 hr. p.i. - 35%

231-10 (E3⁺ vector) 48hr. p.i. - 11%

FIGURE 20

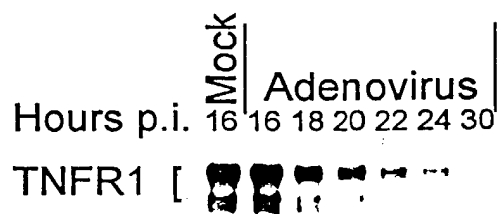


FIGURE 21

09191107089

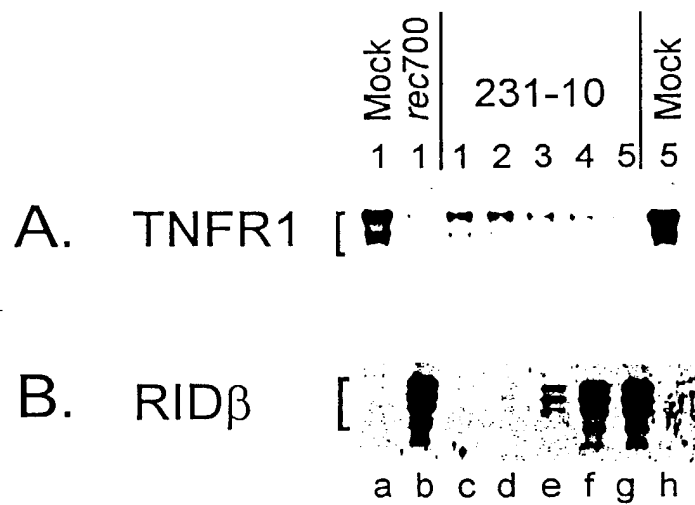


FIGURE 22

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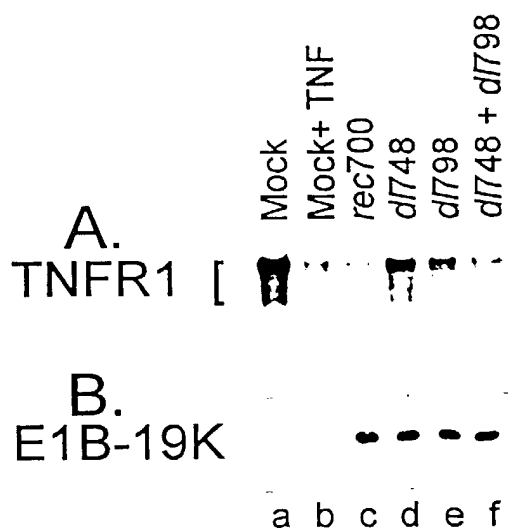


FIGURE 23

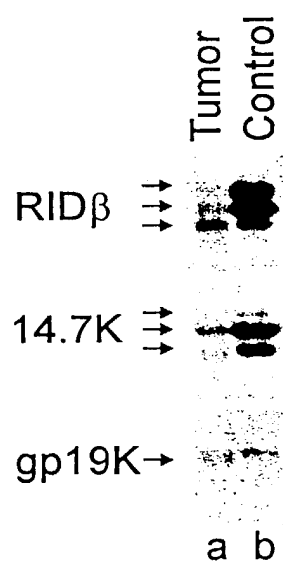


FIGURE 26

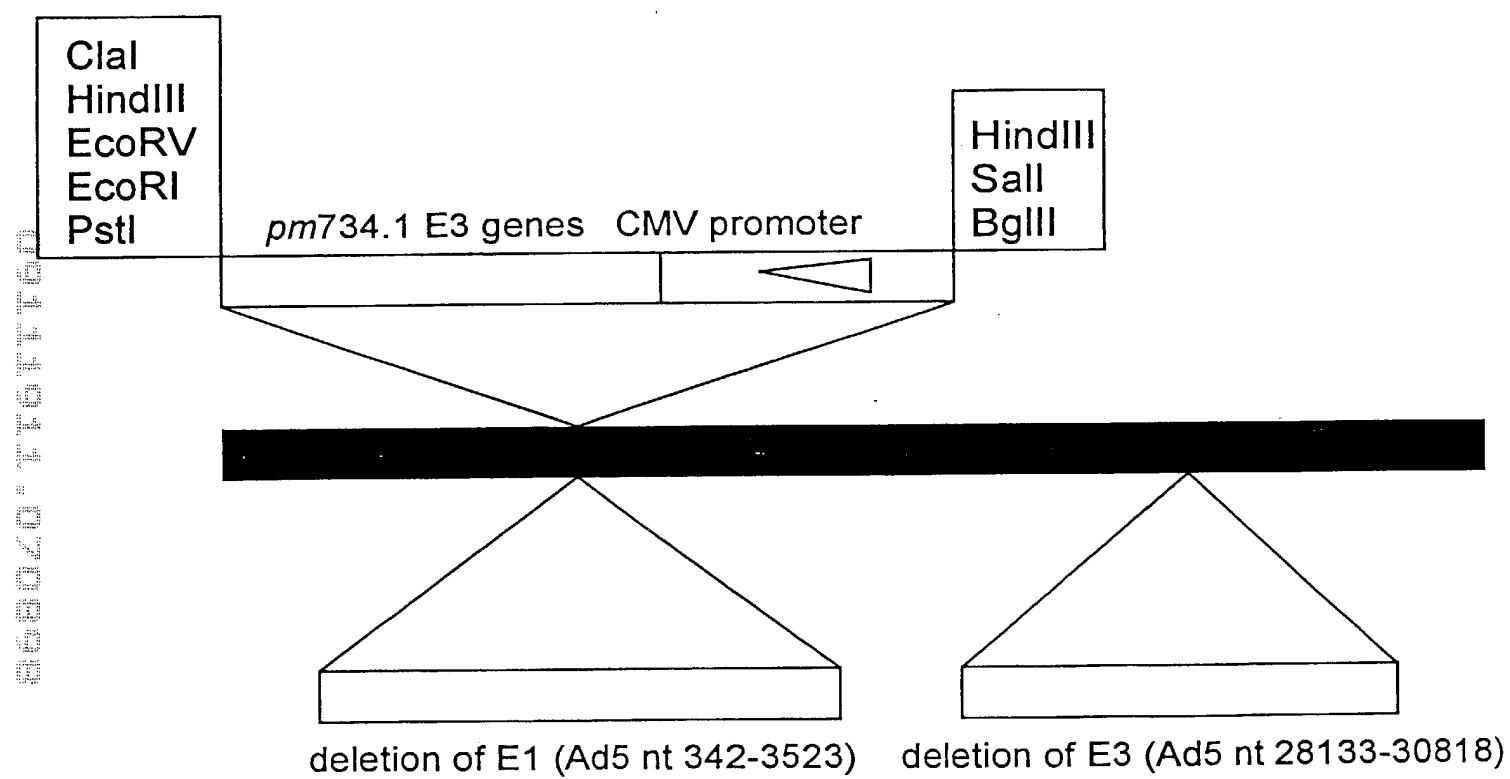


FIGURE 27

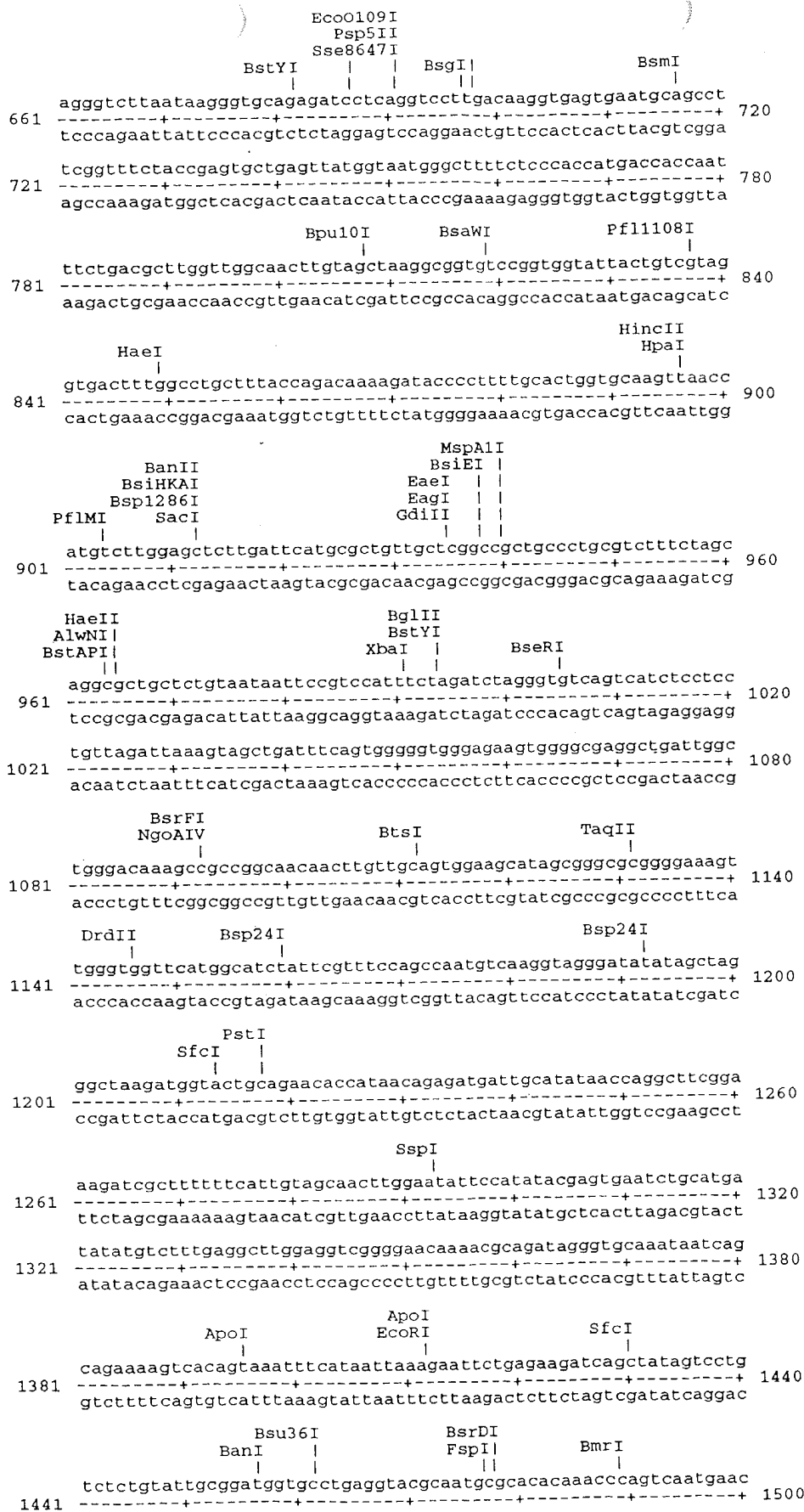


FIGURE 28

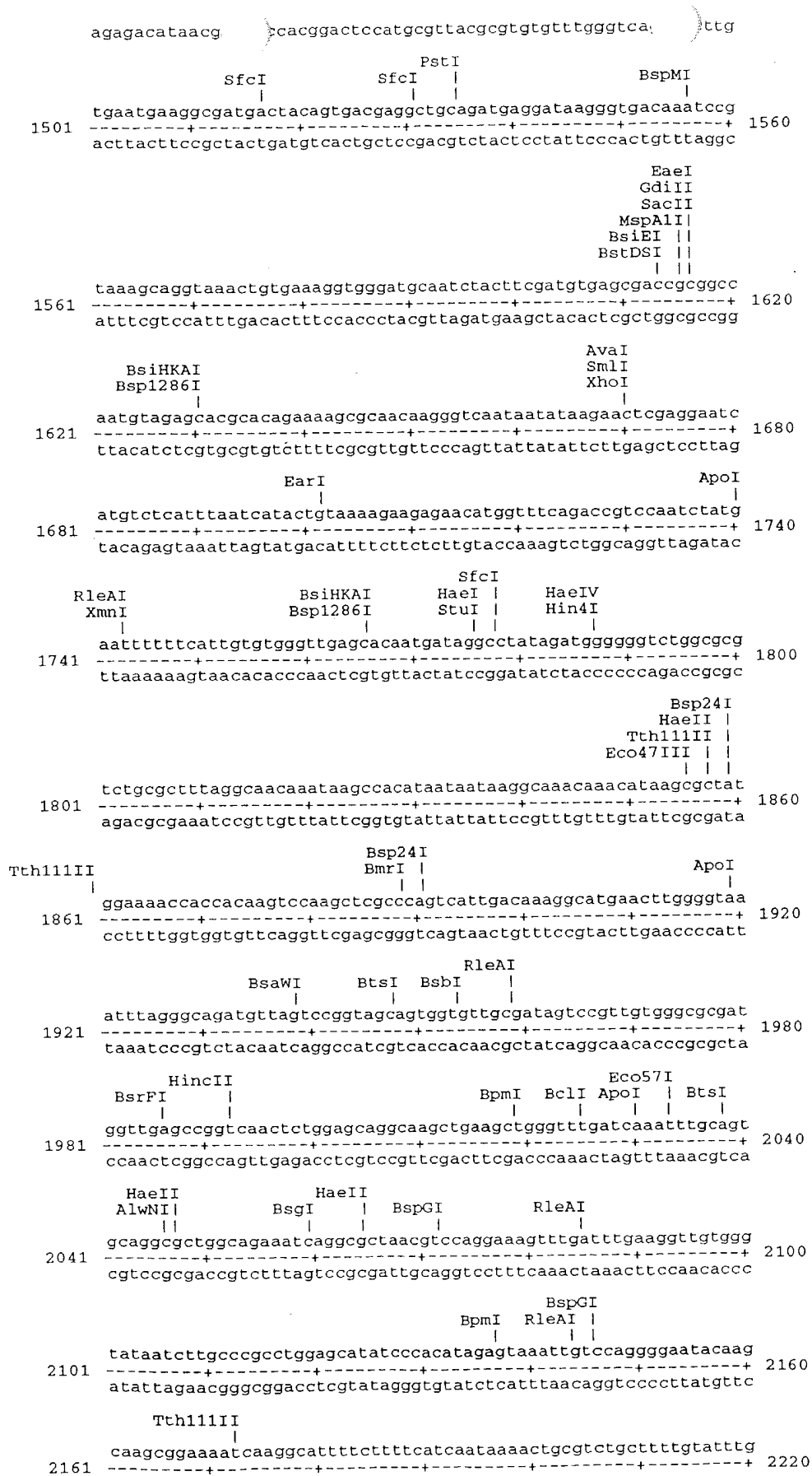


FIGURE 28

gttcgcctttta cgtaaaagaaaagtagttattttgacgcagacgaaa aaac

HaeII
Eco47III | BsrBI BanI

2221 agataaagtaaggtaacataccaaagcaagcgctgtaataagcagagcgggtggaacaaaag 2280
tctatttcattccatgtagtggtttcgttcgcgacattattcgtctcgccacctgttttc

MslI
BsrGI |
TatI |

RleAI MslI Tth111II TatI

2281 gtgccagtgttctctaaacacttttgtgggggccacaacttgactgtttgctcatgtac 2340
cacggtcacaagagatttgtgaaaaacccccgggtgtgaacatgacaaacgagtacatg

ApoI

2341 atggtaatatcgacatttcataaaatggaaatttatacataaaagttttacgattttca 2400
taccattatagcgtgtaaagtattttacctttaaatatgtattttcaaaatgctaaaagt

StyI BbsI DrdI

2401 ccttgggaagactgtgacattatagtcgtagtgacacctggctgccaatagcatataca 2460
ggaaccttctgacactgtaatatcagcaatcacagtgaccgacggtttatcgtatatgt

HindIII

2461 gcataacttgccaattttgtctttgtggcgaataataagcttttcatgttctgtgggtgcat 2520
cgtatgaacgggttaaaacagaaacaccgcttattattcgaaaagtacaagacaccacgta

DraI SwaI BsrDI DrdII

2521 tttataagagtagtgcattcattagcttctgatttaaatgtaacattgcaagctgggtcc 2580
aaatattctcatcacgtaagtaaatcgaagactaaatttacattgtaacgttcgaccaagg

HaeII
SfcI
Eco47III | PstI BglI

2581 ttaaactcaacctttttggcagcgctgcagactgccgcaaggcgagcaagcctaaaatc 2640
aatttgagttggaaaaaccgctcgcgacgtctgacggcggtcccgctcgttcggattttag

DraI BaeI

2641 atgtacctcatcttggatgttggccccagcggtttaaaagctgacaataggtacaaacgt 2700
tacatggagtagaacctacaacgggggtcgcaaatttttcgactgttatccatgtttgca

BsgI
Bsu36I |
BaeI | MslI |

2701 gcgtgcagcagggcggaaccttaaggcacagaagtgttagtataagaataaacagaatta 2760
cgcacgtcgtccgctgtgggattccgtgtcttcacgatcatattcttatttgtctta

HindIII

2761 caagagtaaggataaccccgaccccaattccagaaaaattagacaagctttagaggttac 2820
gttctcattcctattggggctggggttaagggtcttttaattctgttcgaacatctcaatg

PacI

2821 ttgaattgctcatataacttaattaaaaaatcccagcaccgccgaaaatgcttttttgacc 2880
aacttaacgagtatatgaattatttttagggtcggtggggcggttttacgaaaaaactgg

BanII
BsiHKA
Bsp1286I
Hin4I
Hin4I SacI BplI BplI

2881 tgagttccgggagttgagctcacctcctgttttggaaaaatgggagtaatgtctgggtac 2940
actcaaggccctcaactcgagtgaggacaaaacctttttaccctcattacagaccaatg

SfcI
RleAI |
Bpu10I |

BsaWI
BsrFI
PinAI

BspMI
SunI |

AarI |

FIGURE 28



FIGURE 28

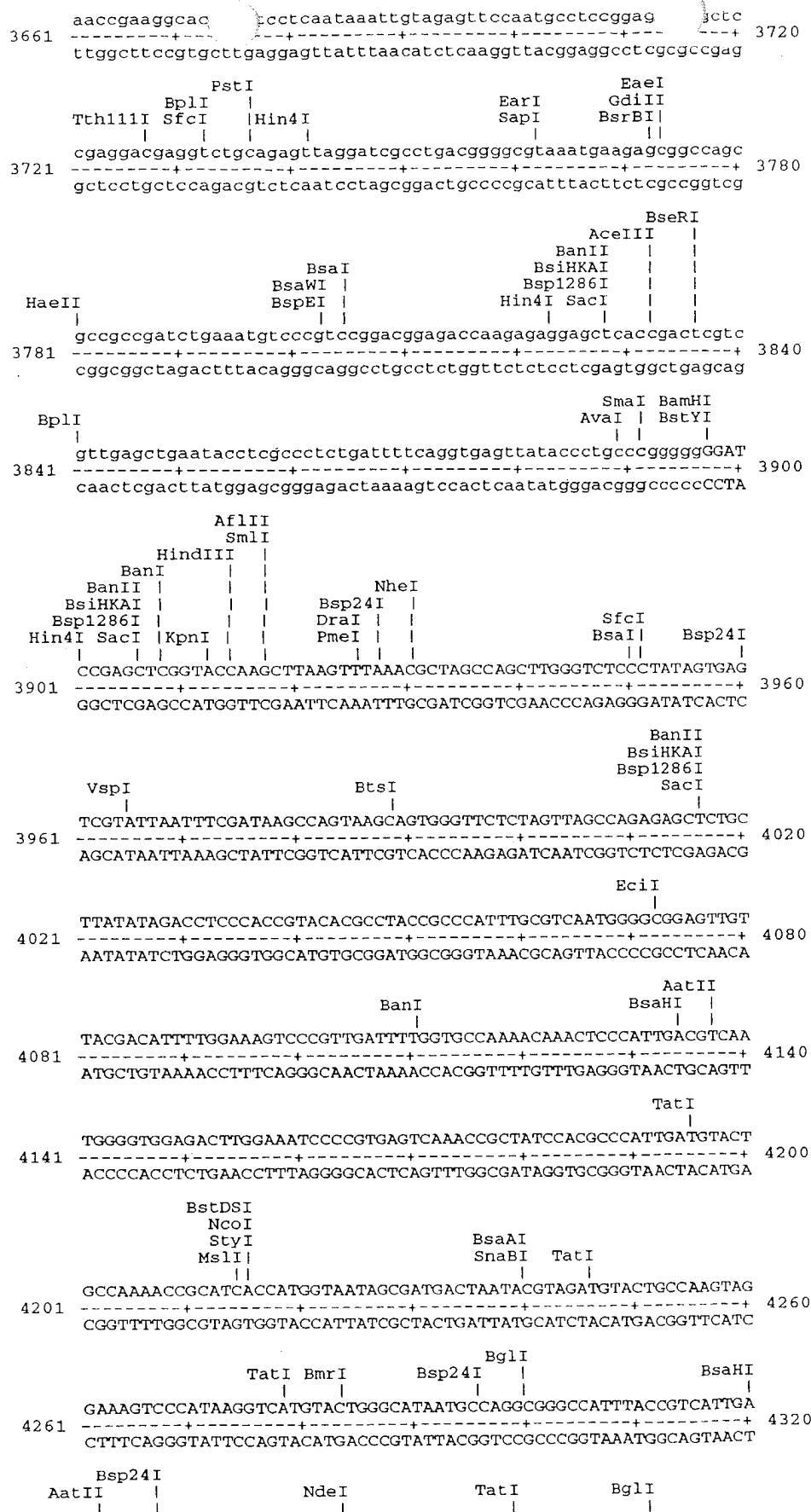


FIGURE 28

CGTCAATAGGGG ACTTGGCATATGATACACTTGATGTACTGCCAAGTG TTTT
 4321 -----+-----+-----+-----+-----+-----+-----+ 4380
 GCAGTTATCCCCCGCATGAACCGTATACTATGTGAAC TACATGACGGTTCACCCGTCAAA

TaqII
 AatII |
 BsaHI | |

ACCGTAAATAGTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAA
 4381 -----+-----+-----+-----+-----+-----+ 4440
 TGGCATTATCAGGTGGGTAAC TGCAGTTACCTTTCAGGGATAACCGCAATGATACCCTT

AatII
 BsaHI | | BglI

CATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGGGCCAT
 4441 -----+-----+-----+-----+-----+-----+ 4500
 GTATGCAGTAATAACTGCAGTTACCCGCCCCCAGCAACCCGCCAGTCGGTCCGCCCGTA

TTACCGTAAGTTATGTAAACGCGGAAC TCCATATATGGGCTATGAACTAATGACCCCGTAA
 4501 -----+-----+-----+-----+-----+-----+ 4560
 AATGGCATTCAATACATTGCGCCTTGAGGTATATACCCGATACTTGATTACTGGGGCATT

AflIII
 MluI
 HincII |
 VspI | SpeI |

TTGATTACTATTAATAACTAGTCAATAATCAATGTCAACGCGTATATCTGGCCCGTACAT
 4561 -----+-----+-----+-----+-----+-----+ 4620
 AACTAATGATAATTATTTGATCAGTTATTAGTTACAGTTGCGCATATAGACCGGGCATGTA

HincII
 Bsp24I
 HindIII |
 NruI | Bpu10I |

CGCGAAGCAGCGCAAAACGCCTAACCCTAAGCAGATTCTTCATGCAATTcaagcttgctcg
 4621 -----+-----+-----+-----+-----+-----+ 4680
 GCGCTTCGTCGCGTTTTCGCGGATTGGGATTTCGTCTAAGAAAGTACGTTAagttcgaacagc

Bsp24I
 BglII |
 BstYI | AflIII |
 SmlI |

acagatcttgggctggccttaaggggtgggaagaatatataaggtgggggtcttatgtag
 4681 -----+-----+-----+-----+-----+-----+ 4740
 tgtctagaaccgcgcaacgaattccaccctttcttatatattccacccccagaatacatc

BsiHKAI
 Bsp1286I

ttttgtatctgttttgcagcagccgcccgcgcatgagcaccactcgtttgatggaagc
 4741 -----+-----+-----+-----+-----+-----+ 4800
 aaaacatagacaaaaagtcgctcgccggcgccggtactcgtggtgagcaaacctaccttcg

BstDSI
 NcoI
 StyI
 BanII |
 BsiHKAI |
 Bsp1286I |
 SacI | NspI |
 SphI | BpmI

attgtgagctcatatttgacaacgcgcgatgcccccatgggcccgggtgcgctcagaatgtg
 4801 -----+-----+-----+-----+-----+-----+ 4860
 taacactcgagtataaaactgttgccgctacgggggtacccggccccacgcagctcttacac

Pfl1108I
 BsaI |
 Bsp24I |
 BanII |
 Bsp1286I |

atgggctccagcattgatggtcgccccgctcctgccccgaaactctactaccttgacctac
 4861 -----+-----+-----+-----+-----+-----+ 4920
 taccgcaggtcgtaactaccagcggggcaggacgggcttgagatgatggaactggatg

PstI
 Eco57I |
 SfcI |
 Bsp24I | | EciI |
 Tth111I |
 Hin4I |
 MmeI |

gagaccgtgtctggaacgcggttgagactgcagcctccgcccgcgcttcagccgctgca
 4921 -----+-----+-----+-----+-----+-----+ 4980
 ctctggcacagaccttgccgcaacctctgacgtcggagggcgccggaagtcggcgacgt

BstAPI
 BtsI
 Bsp1286I
 Bpu10I |
 BanII |
 MspAII |
 BstDSI |
 SacII |

gccaccgccccgaggattgtgactgactttgtcttctgagcccgcttgcaagcagtgca
 4981 -----+-----+-----+-----+-----+-----+ 5040
 cgggtggcgggcgccctaactgactgaaacgaaaggactcgggcgaacgttcgtcacgt

BsgI

FIGURE 28

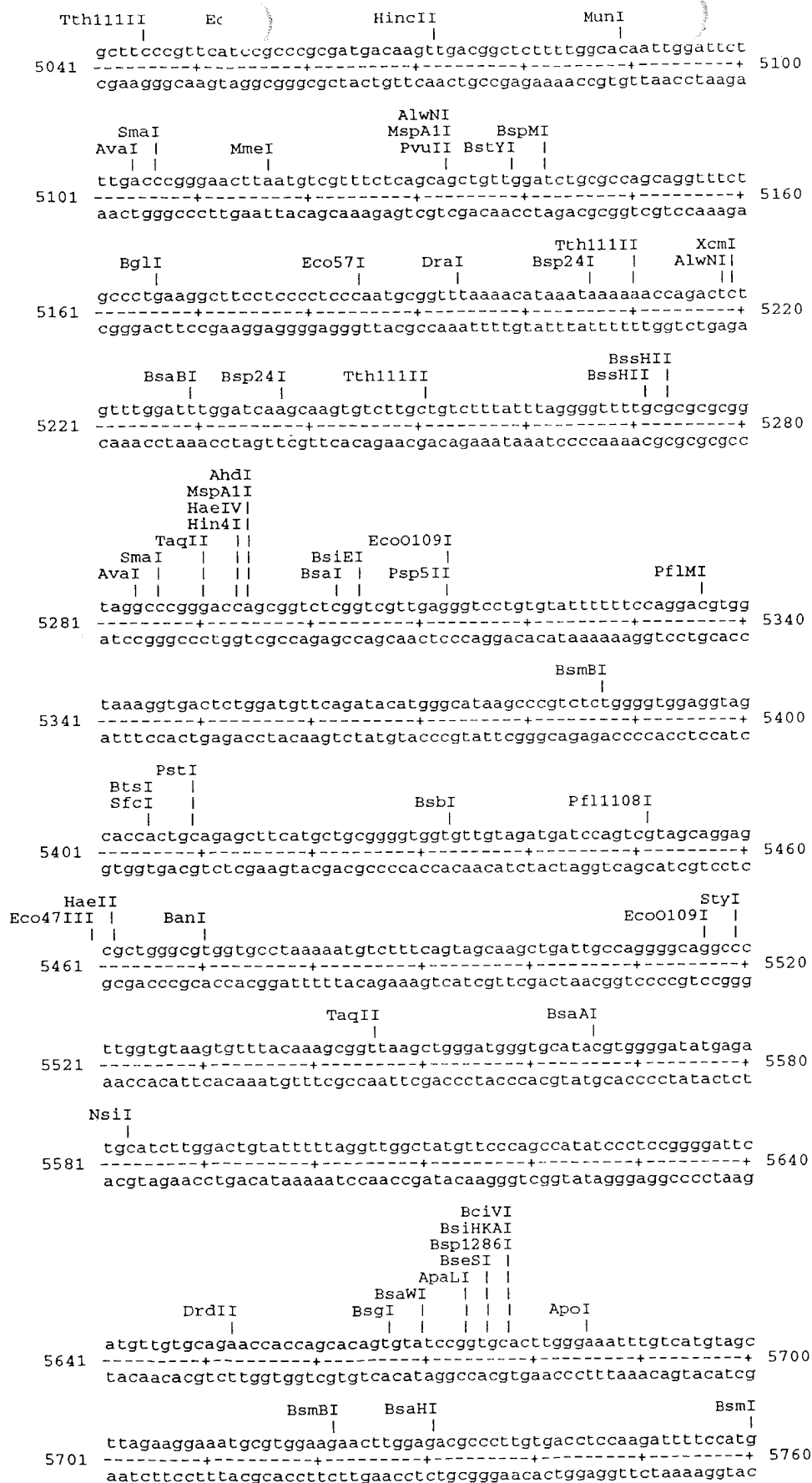


FIGURE 28

ApaI
 BanII
 Bsp1286I
 BstDSI
 BmgI |
 BseSI |
 BsrDI |
 NsiI |
 BstXI |
 MslI |
 5761 cttcgtccataatgatggcaatgggcccacggcgccgctgggcgaagatatcttg 5820
 gtaagcaggtattactaccgttacccgggtgcccgcgcgggacccgcttctataaagac
 MslI | HaeI |
 5821 ggatcactaacgtcatagtgtgttccaggatgagatcgatcaggccatttttacaag 5880
 cctagtgttgtagtatacaacaagggtcctactctagcagtatccggtaaaaaatgtttc
 EciI | BanI | DrdII |
 5881 cgccggcgagggtgccagactcggtataatggttccatccggcccaggggcgtagtta 5940
 gcgcccgcctcccacggtctgacgccattatccaaggtaggccgggtcccgcgcatcaat
 AccI |
 5941 cctcacagatttgcatttcccacgctttgagttcagatggggggatcatgtctacctgc 6000
 gggagtggtctaaacgtaaaagggtgcgaaactcaagtctacccccctagtagcagatggacg
 BspMI | MspAII | PvuII |
 6001 gggcgcatgaagaaaacggtttccggggtaggggagatcagctgggaagaaagcaggttc 6060
 ccccgctacttcttttgccaaaggcccccctcccctctagtcgaccccttctttcgtccaag
 ApaI
 BanII
 Bsp1286I
 BmgI |
 BseSI |
 Bpu10I | MspAII | PvuII | BsrFI | HgiEIII |
 6061 ctgagcagctgacgacttacgcagccgggtgggcccgtaaatcacacctattaccgggtgc 6120
 gactcgctgacgctgaatggcgctcgccacccgggcatttagtggtgataatggcccacg
 MspAII | PvuII | PstI |
 AceIII | SfcI | Bpu10I |
 6121 aactggtagttaagagagctgcagctgcccgtcatccctgagcagggggccacttcgta 6180
 ttgaccatcaattctctcgacgtcgacggcagtagggactcgccccccggtgaagcaat
 NspI | NspI | EciI | HaeII |
 6181 agcatgtccctgactcgcatgttttccctgaccaaataccgccagaaggcgctcgccgccc 6240
 tcgtacagggactgagcgtacaaaaggactggttaggcggtcttccgcgagcgcggg
 BstAPI | BsaI | EciI |
 6241 agcgatagcagttcttgcagggaagcaaagtttttcaacggtttgagaccgtccgcccga 6300
 tcgctatcgtaagaacgttccttcgtttcaaaaagttgccaactctggcaggcgccat
 NspI | SphI | TaqII | RleAI | AceIII |
 Tth111III | BstEII | AarIII |
 6301 ggcatgcttttgagcgtttgaccaagcagttccaggcgggtcccacagctcggtcacctgc 6360
 ccgtacgaaaactcgcaaaactggttcgtcaaggtccgcccagggtgctgagccagtggaacg
 BspMI | BseRI |
 6361 tctacggcatctcgatccagcatatctcctcggtttcgcggttggggcggtttcgctgt 6420
 agatgccgtagagctaggctgtatagaggagcaaagcgcccaaccccgccgaaagcgaca
 BspGI | BsiHKAI | Bsp1286I | BstDSI | BcgI | EcoO109I | Psp5II |
 6421 acggcagtagtcgggtgctcgtccagacgggcccagggtcatgtctttccacgggcgaggg 6480

FIGURE 28

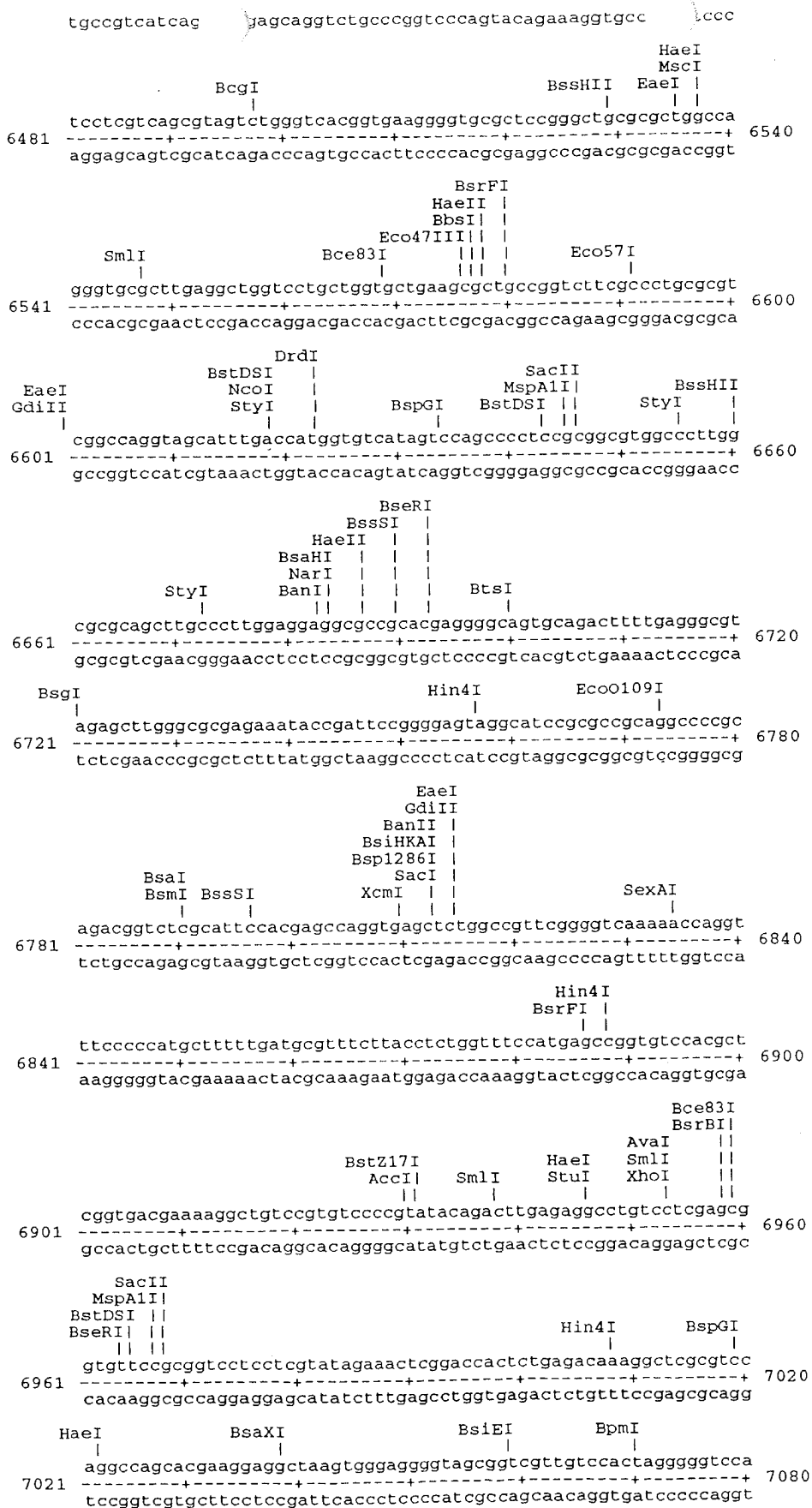


FIGURE 28

[illegible]

FIGURE 28

SmaI
 AvaI | BssHII
 7741 taaagaccccgggcagcagcgcgcgctcgaagtagtctatcttgcatccttgcaagtcta 7800
 atttctggggccgctcgctccgcgcgagcttcacatagatagaacgtaggaacgttcagat
 BstDSI
 EcoO109I |
 Psp5II NcoI
 HaeII BssHII BssHII | SanDI StyI
 7801 gcgctgctgcatgcgcgggcggaagcgcgcgctcgatgggttgagtgggggacccc 7860
 cgcgagcagcggtacgcgcccgcttcgcgcgcgagcataccaactcaccctcgggg
 PflMI
 TaqII | NspI | Hin4I
 7861 atggcatgggggtgggtgagcgcgaggcggtacatgccgcaaatgtcgtaaacgtagaggg 7920
 taccgtacccacccactcgcgcccgcatgtacggcggttacagcatttgcatctccc
 SacII
 MspAII |
 BstDSI | BssHII
 BanII Bsp1286I BpII
 7921 gctctctgagtagttccaagatatgtaggtagcatcttcaccgcggatgctggcgcgca 7980
 cgagagactcataaggttctatacatcccatcgtagaaggtggcgccctacgaccgcggt
 BsaAI BseRI TaqII
 7981 cgtaatcgtagtctcgtagcgaggagcgaggaggtcgggaccgaggttgctacggggcg 8040
 gcattagcatatcaagcacgctccctcgctcctccagccctgggtccaacgatgcccgcc
 MmeI NspI
 BbsI | MmeI | Eco57I
 8041 gctgctctgctcggaagactatctgcctgaagatggcatgtgagttggatgatatggttg 8100
 cgacgagacgagccttctgatagacggaacttctaccgtacactcaacctactataccaac
 BsaI
 BbsI BsaHI |
 8101 gacgctggaagacgttgaagctggcgctctgtgagacctaccgctcacgcacgaaggagg 8160
 ctgcgaccttctgcaacttcgaccgcagacactctggatggcgagtgctgcttctctcc
 BsgI AceIII BspMI
 HincII | BstEII | DrdI |
 8161 cgtaggagtcgcgagcttgttgaccagctcgggcggtgacctgcacgtctagggcgagtg 8220
 gcatcctcagcgcgctcgaacaactggctcgagccgcaactggacgtgcagatcccgcgctca
 BspGI
 8221 agtccagggttttcttgatgatgtcatacttatacttcttcttcttcttccacagctcgc 8280
 tcagggtcccaaggaactactacagtatgaataggacagggaaaaaaagggtgtcgagcg
 ScaI
 AceIII EarI | TatI |
 8281 gggtgaggacaaaactcttcgcggtctttccagtactcttgatcggaaccgctcggcct 8340
 ccaactcctggttgagaagcgccagaaggtcatgagaacctagcctttgggagccgga
 NspI HincII BglI
 8341 ccgaacggtaagagcctagcatgtagaactggttgacggcctggtaggcgagcatccct 8400
 ggcttgccattctcggtcgtagcatcttgaccaactgccggaccatccgcgtcgtaggga
 TaqII
 RleAI |
 BsaWI |
 BglI BspEI |
 8401 tttctacgggtagcgcgctatgctcgcgccgcttcgggagcgaggtgtgggtgagcgcaa 8460
 aaagatgcccatcgcgcatagcgacgcgccggaaggcctcgctccacacccactcgcggt
 EciI
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FIGURE 28

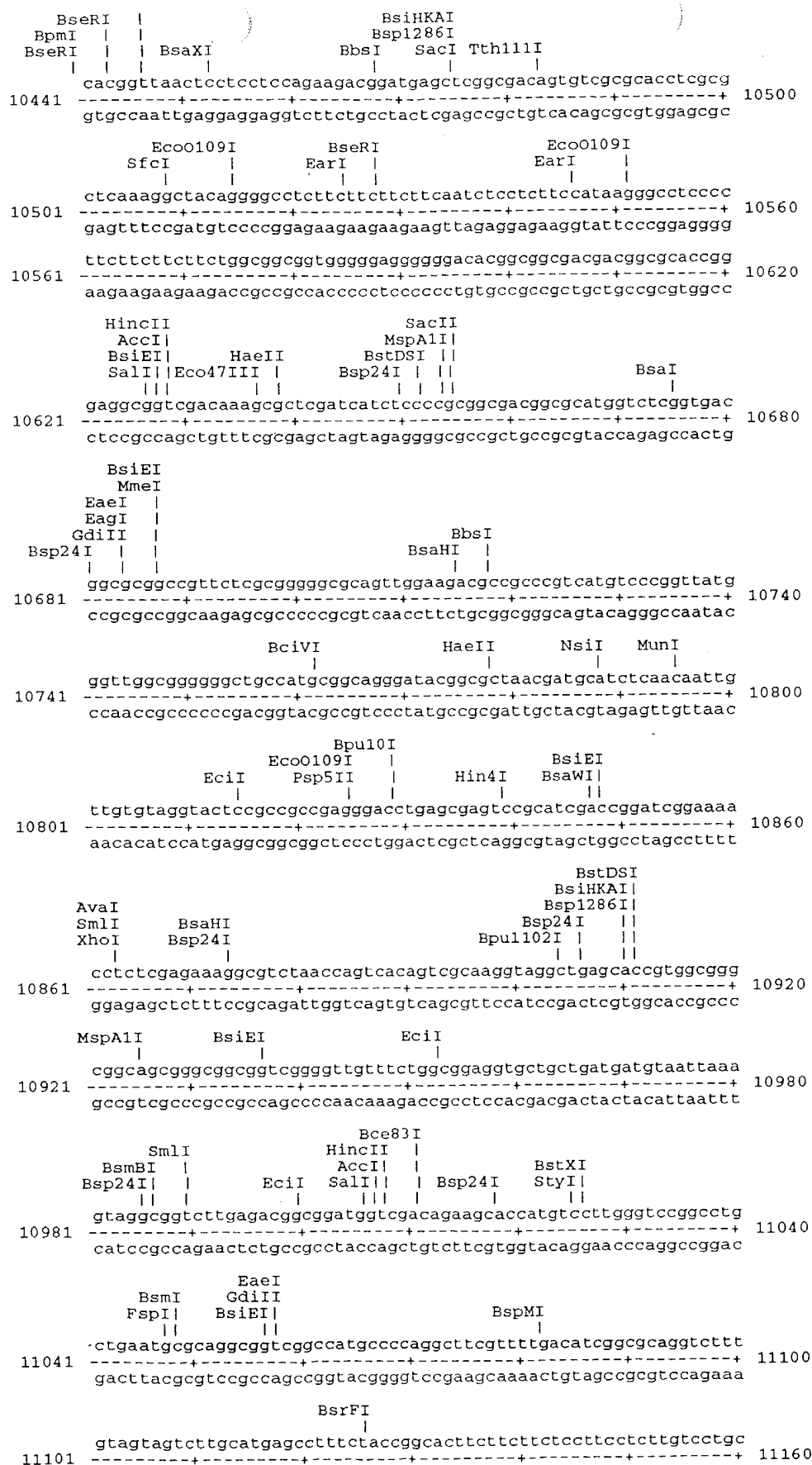


FIGURE 28

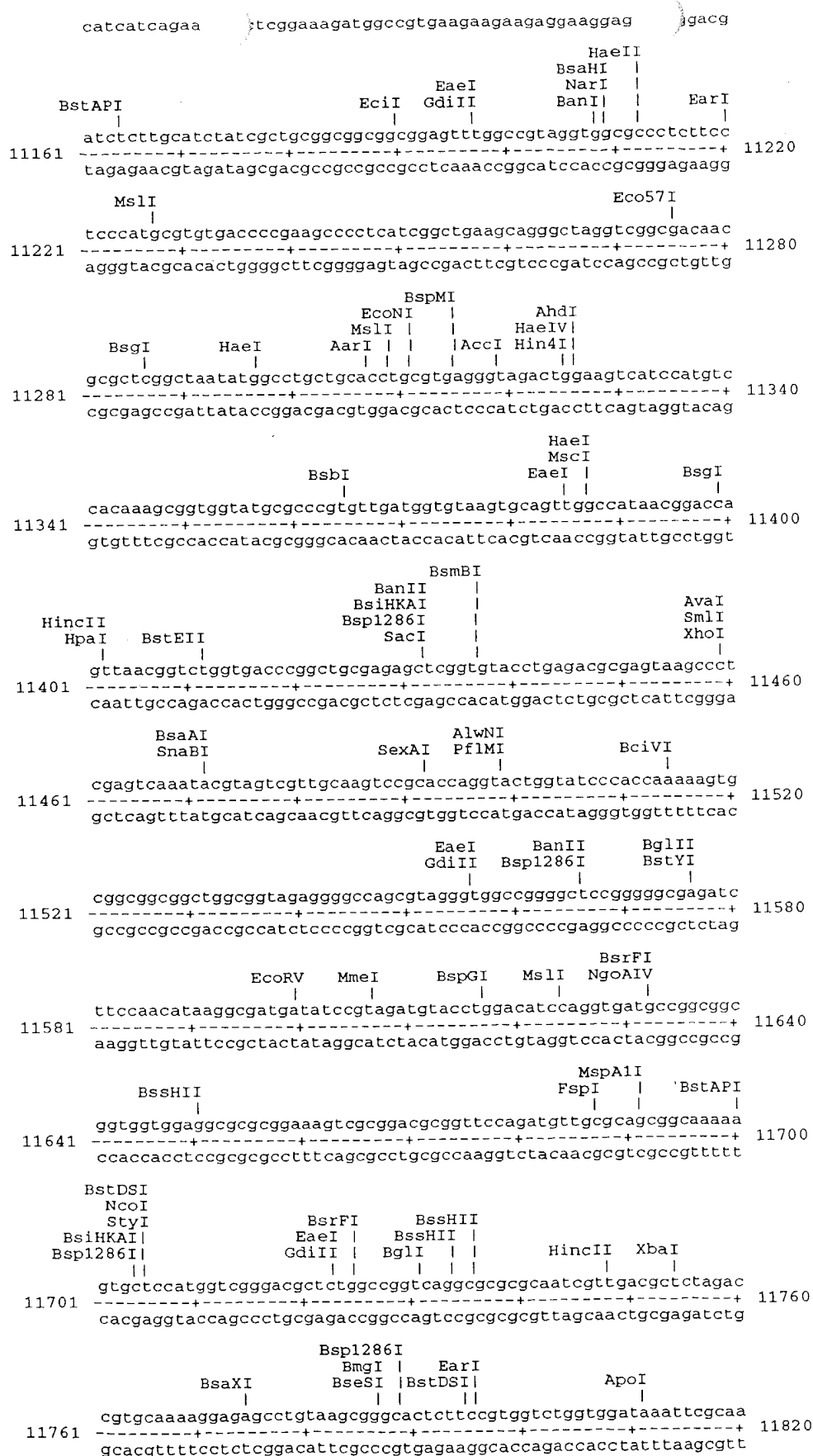


FIGURE 28

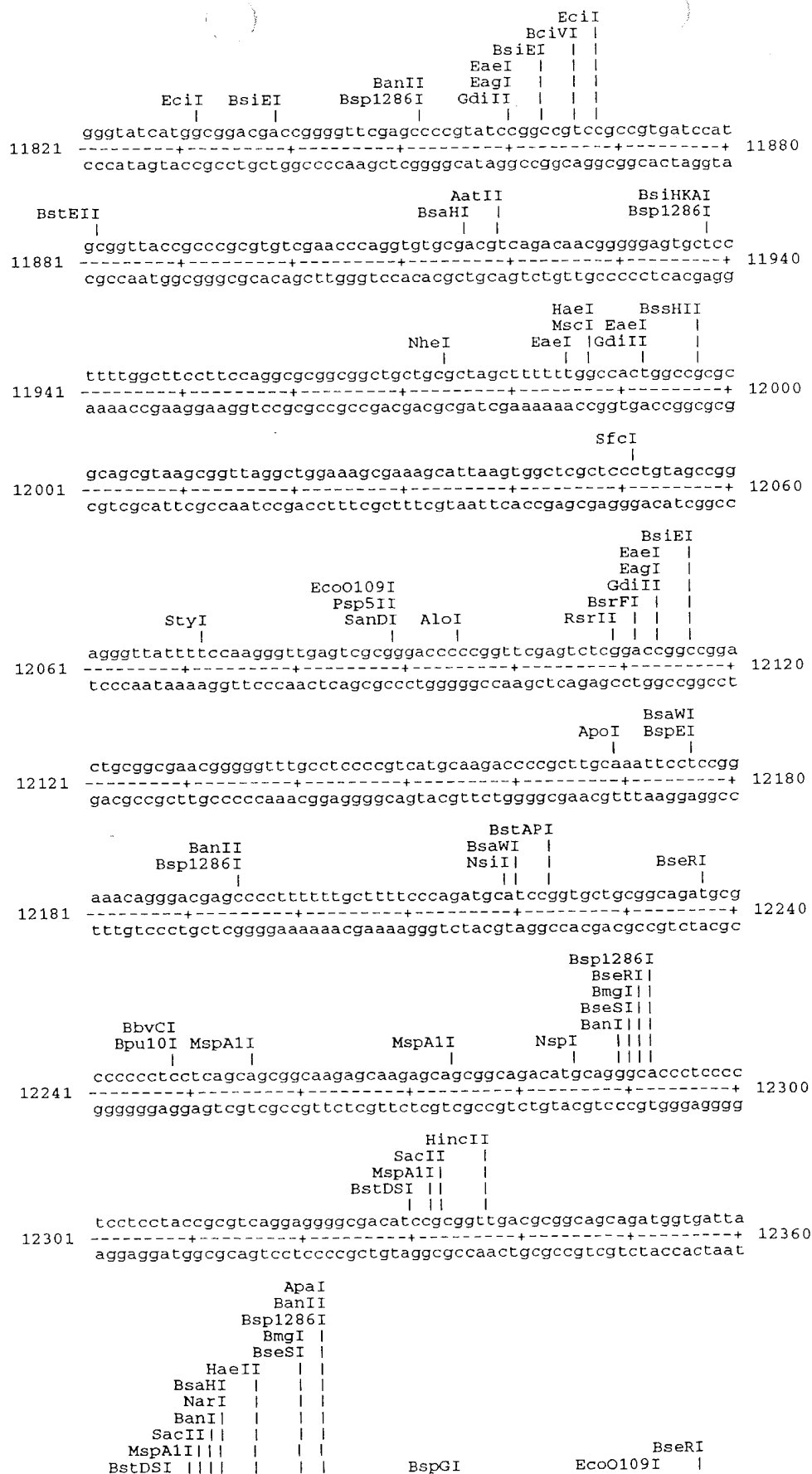


FIGURE 28

12361 cgaacccccgcg_ ccgggccccgcactacctggacttgaggaggcgag_ actggc 12420
gcttggggggcgccgcggcccgccgctgatggacctgaacctcctcccgctcccggaaccg

BanI BsrBI StyI MspAII BsgI
HaeII Bpu10I KpnI PvuII AflIII MluI
gctggctaggagcgccctctcctgagcgggtacccaagggtgcagctgaagcgtgatacgcg 12480
cgccgatcctcgcgggagaggactcgccatgggttcccacgtcgacttcgcactatgcgc

SacII MspAII BstDSI
BsaAI SunI AlwNI NruI BsiEI BanII Bsp1286I
Eco57I AvaI
tgaggcgctacgtgccgcgcgacacctgttccgcgacgcgagggagaggagcccgagga 12540
actccgcgatgcacggcgccgtcttggacaaagcgtggcgctccctctcctcgggctcct

HaeIV Hin4I AhoI BseRI BsrBI
BseRI BseRI AceIII HaeI NruI
gatgcgggatcgaaagttccacgcagggcgagctgcggcatggcctgaatcgcgagcg 12600
ctacgccttagctttcaagtgctcccgctcgacgccgtaccggacttagcgctcgc

BanII Bsp1286I BssHII
BseRI BssHII
gttgctgcgcgaggaggactttgagcccgacgcgcgaaccgggattagtcgcgcgcgcg 12660
caacgcgcgcgtcctcctgaaactcgggctgcgcgcttggccctaatacaggcgcgcgcg

BsiEI EaeI EagI GdiII
BsaAI PmlI BstEII DrdII
AflIII NotI SexAI
acacgtggcgccgcgcgacctggtaaccgcatacagcagacgggtgaaccaggagattaa 12720
tgtgcaccgcgcggcggtggaccattggcgctatgctcgtctgccacttggctcctctaatt

SunI HindIII BsaAI PmlI BssHII SfcI
ctttcaaaaaagctttaacaaccagctgcgtacgcttggcgcgcgaggaggtggctat 12780
gaaagtttttctgaaattgttgggtgcacgcacatgcgaacaccgcgcgtcctccaccgata

RleAI BseRI NsiI BssHII BpmI
aggactgatgcatctgtgggactttgtgaagcgcgctggagcaaaacccaaatagcaagcc 12840
tcctgactacgtagacaccctgaaacattcgcgcgacctcgttttgggtttatcggtcgg

BsrBI MspAII PvuII BsmI BsgI
gctcatggcgagctgttccttatagtgacagcacagcagggaacacgaggtcattcagga 12900
cgagtaccgcgtgcacaaggaatatcacgtcgtgctcctcgttgctcgcgtaagtcct

BanII Bsp1286I AvaI MspAII BsaBI SfcI
tgcgctgctaaacatagtagagcccgaggcccgctggctgctcgatttgataaacatcct 12960
acgcgacgatttgtatcatctcgggctcccgcgacccgacgagctaaactattttagga

PstI MslI SmlI BsgI Bce83I EaeI GdiII
gcagagcatagtggtgcaggagcgagcttgagcctggctgacaaggtggcgcccatcaa 13020
cgtctcgtatcaccacgtcctcgcgctgaactcggaccgactgttcacggcggtagtt

FIGURE 28

Xcm
 Bpu1102I
 13021 ctattccatgcttagcctgggcaagttttacgcccgaagatataccataccccttacgt 13080
 gataaggtacgaatcggaaccgttcaaatgcgggcggttctatatggtatggggaatgca
 FspI
 MslI
 NspI HaeII
 13081 tcccatagacaaggaggttaagatcgaggggttctacatgcgcgatggcgctgaaggtgct 13140
 agggatatctgttctccattcttagctcccaagatgtacgcgtaccgcgacttccacga
 SmlI Eco57I Bce83I
 13141 taccttgagcgacgacacctgggcgtttatcgcaacgagcgcatccacaaggccgtgagcgt 13200
 atggaactcgctgctggaccgcgaatagcgttgctcgcgtaggtgttcggcactcgca
 ApaI
 BanII
 Bsp1286I
 BmgI
 BseSI
 EcoO109I
 EcoO109I
 BsrFI
 NgoAIV
 Bpu1102I
 BsiEI
 BstAPI
 13201 gagccggcgcgcgagctcagcgaccgcgagctgatgcacagcctgcaaagggccctggc 13260
 ctgcggcgccgcgctcgagtcgctggcgctcgactacgtgtcggacgtttcccgggaccg
 MspAII Hin4I Bsp24I HaeII
 13261 tggcacgggcagcgcgcatagagagccgagtcctactttgacgcggcgctgacctgcg 13320
 accgtgcccgtcgccgctatctctccggctcaggatgaaactgcgcccgcgactggacgc
 ApaI
 BanII
 Bsp1286I
 Bsp24I
 BmgI
 BseSI
 EcoO109I
 BspMI
 Bsp24I
 BglI
 PvuII
 BpmI
 BanI
 13321 ctgggcccgaagccgacgcgccttgaggcagctggggccggacctgggctggcggtggc 13380
 gaccgggggttcggctgcgcgggacctccgtcgaccccgccctggacccgacccgacccg
 BssHII
 Bsp24I
 BssHII
 13381 acccgcgcgcgctggcaacgtcgcgggcggtggaggaatatgacgaggacgatgagtacga 13440
 tggggcgcgcgacccgttgacgcgcgcacctccttatactgctcctgctactcatgct
 ScaI
 TatI
 BclI
 13441 gccagaggacggcgagtagtaagcgggtgatgtttctgatcagatgatgcaagacgcaacg 13500
 cggctcctctgcgctcatgattcgccactacaagactagtctactacgttctgcgttgc
 PstI
 HaeII
 SfcI
 BstDSI
 13501 gaccggcggtgcgggcgcgctgcagagccagccgtccggccttaactccacggacgac 13560
 ctggggccgcacgcgcgcgacgtctcggtcggcaggccggaattgaggtgcctgctg
 HaeII
 BsaHI
 NarI
 BanI
 PflMI
 BssHII
 AflIII
 MluI
 13561 tggcgccaggtcatggaccgcatcatgtcgctgactgcgcgcaatcctgacgcgttcgg 13620
 acccggtccagtaacctggcgtagtacagcgactgacgcggttaggactgcgcaaggcc
 BsaXI
 BsrFI
 HaeI
 BssHII
 BssHII
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FIGURE 28

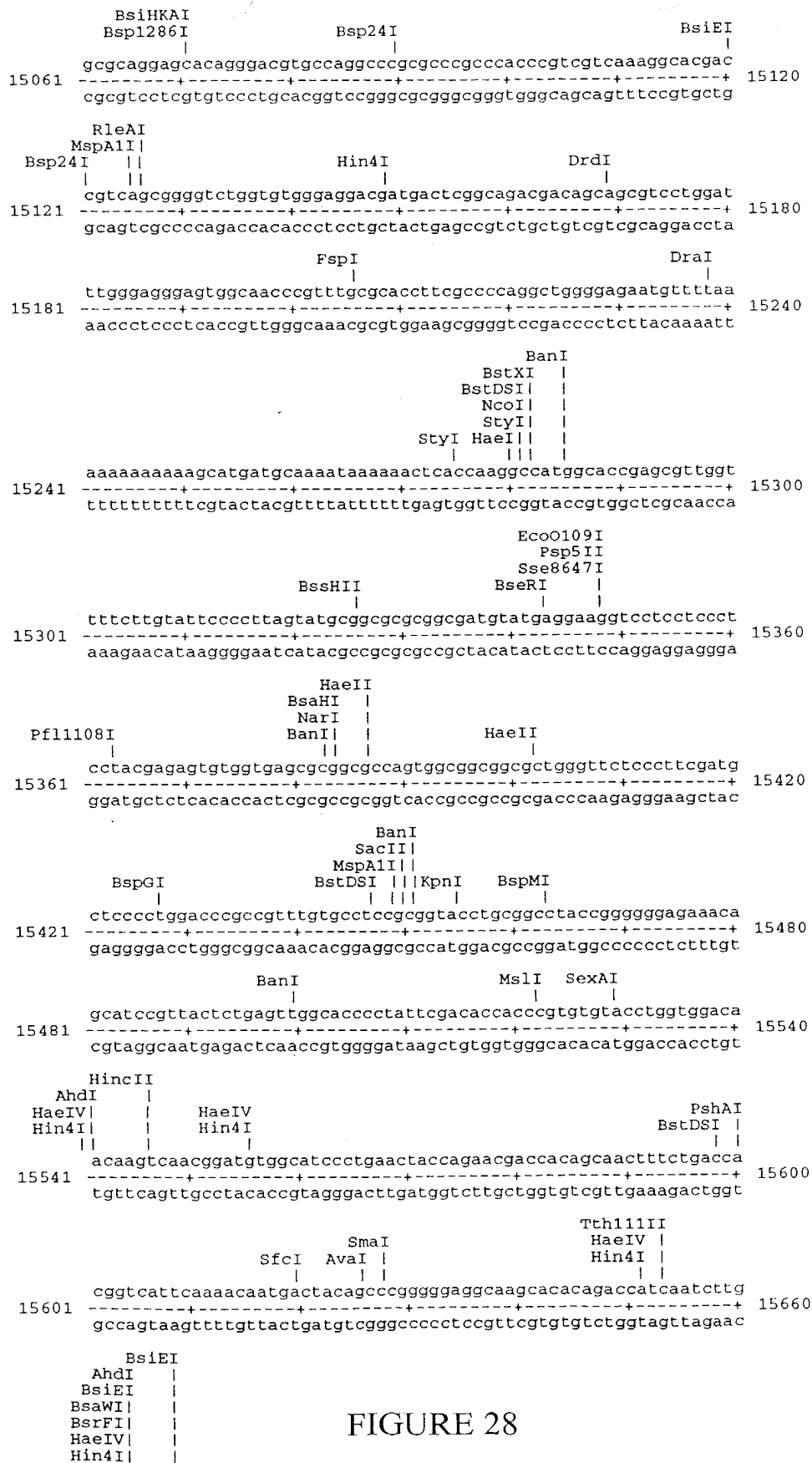


FIGURE 28

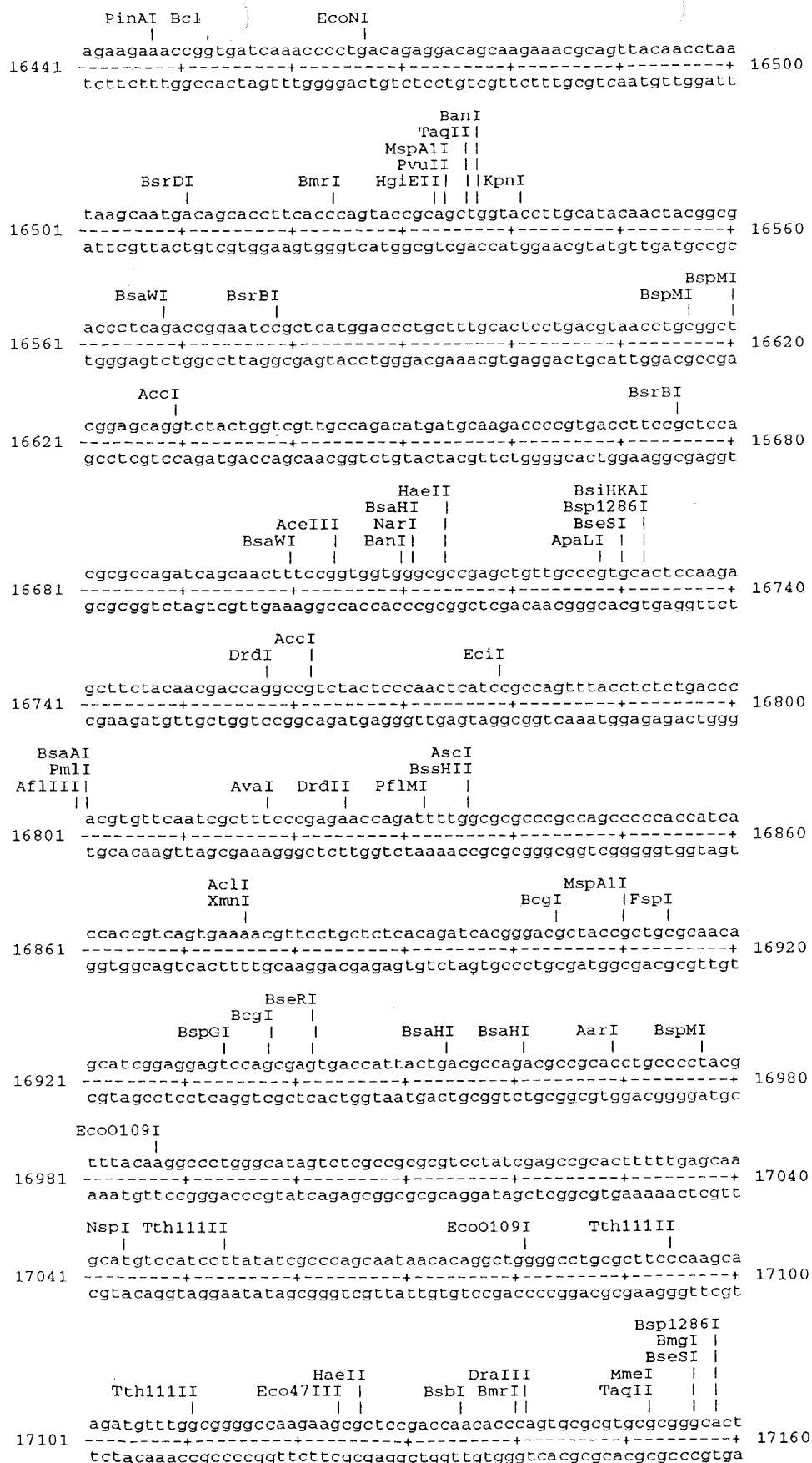


FIGURE 28

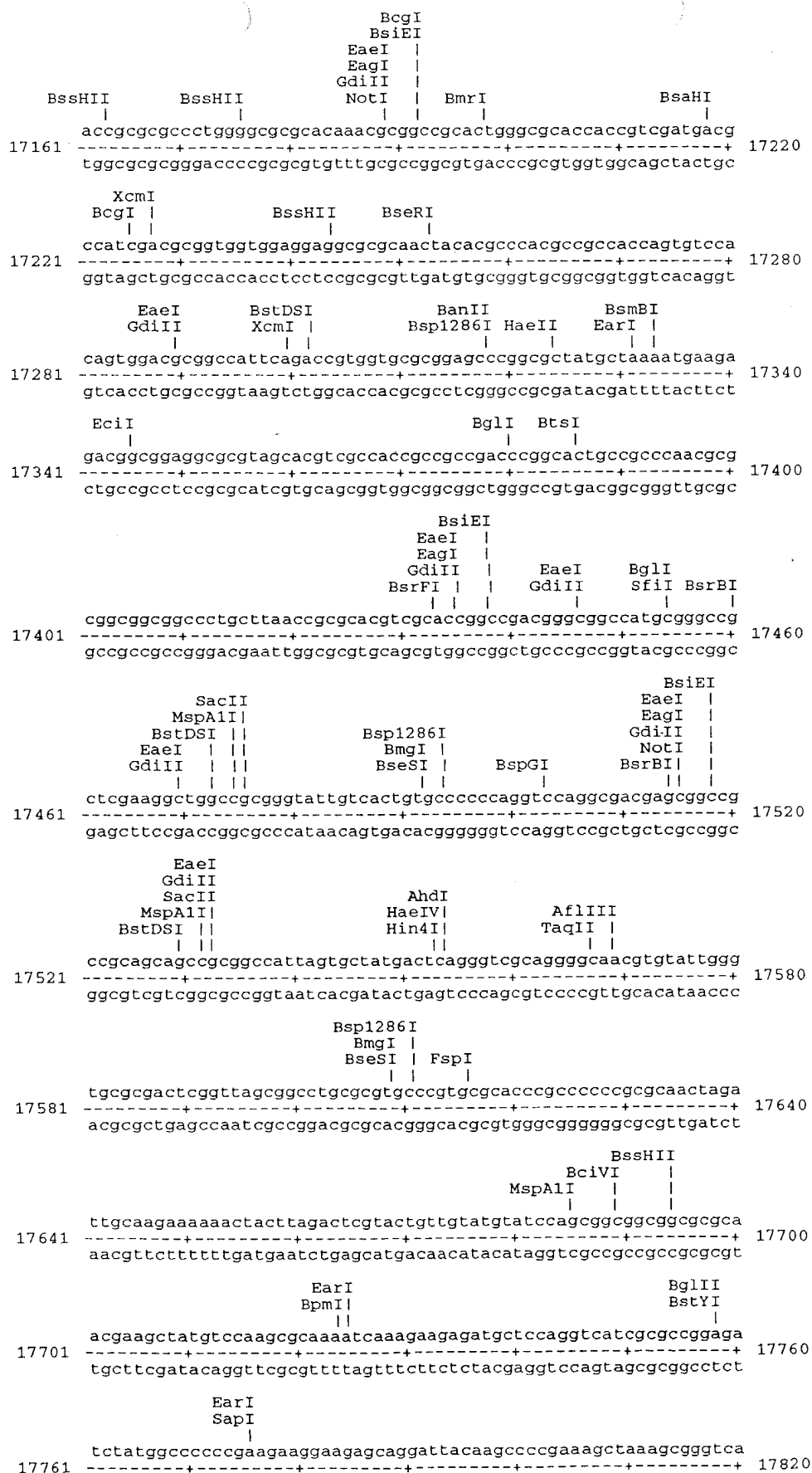


FIGURE 28

agataaccgggg cttccttctcgtcctaagtgttcggggctttcgatt ccagt

BspI

17821 +-----+-----+-----+-----+-----+ 17880

aaaagaaaaagaaagatgatgatgaacttgacgacgaggtggaactgctgcacgcta
 ttttctttttcttttctactactacttgaactgctgctccacttgacgacgtgcat

AflIII
 MluI
 HincII |
 AccII |
 SalII || | AflIII BanI

17881 +-----+-----+-----+-----+-----+ 17940

ccgcgcccaggcgacgggtacagtggaaaggtcgacgcgtaaaacgtgttttgcgacccg
 ggcgcggttcgctgcccattgtcacctttccagctgcatgtttgcacaaaacgctgggc

HaeII
 Eco47III |

17941 +-----+-----+-----+-----+-----+ 18000

gcaccaccgtagtcttttacgcccgtgagcgctccaccgcacctacaagcgctgtatg
 cgtggtggcatcagaaatgcgggccactcgcgaggtggcggtgatgttcgcgcacatac

EcoO109I Psp5II BspMI AvaI
 Sse8647I SmlI HaeI Bce83I
 Tth111III | | | HaeII |

18001 +-----+-----+-----+-----+-----+ 18060

atgaggtgtacggcgacgaggacctgcttgagcaggccaacgagcgcttcggggagtttg
 tactccacatgccgctgctcctggacgaactcgtccggttgctcgcgagccctcaaac

NspI BspGI BspI
 MspAII | | |

18061 +-----+-----+-----+-----+-----+ 18120

cctacggaaagcggcataaggacatgctggcggttgccgctggacgagggcaacccaacac
 ggatgccttttcgccgtattctctgtacgacgcaacggcgacctgctcccggtgggttggtg

AlwNI
 BstAPI
 BtsI AarI |
 SfcI BstAPI |
 BspMI PstI |

18121 +-----+-----+-----+-----+-----+ 18180

ctagcctaaagccgtaaacactgcagcaggtgctgcccgcttgcccgctccgaagaaa
 gatcggttttcgggcattgtgacgtcgtccacgacggcgcaacgtggcaggtctctt

BanI
 TaqII |
 MspAII | |
 PvuII | | KpnI

18181 +-----+-----+-----+-----+-----+ 18240

agcgcgccctaagcgcgagtcctggtgacttgccacccaccgtgcagctgatggtagccca
 tcgcgccggtatttcgctcagaccactgaaccgtgggtggcacgtcgactaccatgggt

HaeII AlwNI BanII
 BspI | PflMI Bsp1286I
 BstDSI AvaI |

18241 +-----+-----+-----+-----+-----+ 18300

agcgccagcgactggaagatgtcttggaaaaaatgaccgtggaacctgggctggagcccg
 tcgcggtcgctgaccttctacagaacctttttactggcaccttggaacccgacctcgggc

Tth111III
 HaeII |
 BspMI BsaHI |
 BpmI | NarI |
 EaeI | BanI |
 GdiII | AarI | BmrI BstDSI

18301 +-----+-----+-----+-----+-----+ 18360

aggtccgctgcccgaatcaagcaggtggcgccgggactggcgctgcagaccgtggacg
 tcaggcgcacgcgggttagttcgtccaccgcccctgaccgcacgtctggcacctgc

BspI XcmI

18361 +-----+-----+-----+-----+-----+ 18420

ttcagataccactaccagtagcaccagatttgccaccgccagagggcatggagacac
 aagtctatgggtgatgggtcatcgtggtcataacggtggcggtgtctcccgtaacctctgtg

BspI
 BsiEI |
 EaeI | |
 EagI | |
 GdiII | |

MspAII SacII BstDSI

BbvCI | | |

FIGURE 28

DrdI B EciI BsiEI
 | | | |
 18421 aaacgtccccgggttgctcagcgggtggcggatgcgcgggtgcaggcggctcgtgcggccg 18480
 -----+-----+-----+-----+-----+-----+-----+-----+
 ttgcagggggccaacggagtcgccaccgcctacggcgccacgtccgccagcgacgccggc

 BstDSI
 |
 18481 cgtccaagacctctacggaggtgcaaacggaccgctggatgtttcgcggtttcagccccc 18540
 -----+-----+-----+-----+-----+-----+-----+-----+
 gcaggttctggagatgcctccacgtttgcctgggcacctacaaagcgcaaagtcgggggg

 HaeII HaeII
 BsaHI | BsaHI |
 NarI | NarI |
 BanI | BanI | BssHII
 | | |
 18541 ggcgcccgcgcggttcgaggaagtacggcgccgcagcgctactgcccgaatatgcc 18600
 -----+-----+-----+-----+-----+-----+-----+-----+
 ccgcgggcgcgccaagctccttcatgccgcggcggtcgcgcgatgacgggcttatacggg

 BsrDI
 |
 18601 tacatccttccattgcgcctacccccggctatcgtggctacacctaccgccccagaagac 18660
 -----+-----+-----+-----+-----+-----+-----+-----+
 atgtaggaaggtaacgcggatgggggcccgatagcaccgatgtggatggcggggtcttctg

 BbsI BsaHI DrdII
 | | |
 18661 gagcaactaccgcagccgaaccaccactggaaccgcgcgcgcgtcgccgtcgccagc 18720
 -----+-----+-----+-----+-----+-----+-----+-----+
 ctcggttgatgggtgcggcttggtggtgacctggggcgcgcgccagcgccagcggtcg

 BcgI FspI NruI EcoO109I
 | | | |
 18721 ccgtgctggccccgatttccgtgcgcagggtggctcgcgaaggaggcaggaccctgggtgc 18780
 -----+-----+-----+-----+-----+-----+-----+-----+
 ggcacgaccggggctaaaggcacgcgtcccaccgagcgcttctcgtcctgggaccacg

 BssHII BsrFI DraI DrdII
 | | | |
 18781 tgccaacagcgcgctaccaccccagcatcggtttaaagccggtctttgtggttcttgcag 18840
 -----+-----+-----+-----+-----+-----+-----+-----+
 acggttgctgcgcgatggtggggtcgtagcaaattttcgccagaaacaccaagaacgtc

 AarI BspMI BanI BsmI
 | | | |
 18841 atatggccctcacctgcccctcctggtttcccggtgcccggattccgaggaagaatgcacc 18900
 -----+-----+-----+-----+-----+-----+-----+-----+
 tataccgggagtggaaggcgaggcgaagggccacggccctaaggctccttcttacgtgg

 BstDSI
 FseI
 EaeI
 GdiII
 BsrFI
 NgoAIV
 EaeI
 GdiII
 BglI NspI SphI FspI BsrFI
 | | | | |
 18901 gtaggaggggcatggcggccacggcctgacggggcgcatgcgtcgtgcgcaccaccggc 18960
 -----+-----+-----+-----+-----+-----+-----+-----+
 caccctcccgtaccggccggtgcgggactgcccgcgtacgcagcacgcgtggtggccg

 BssHII NspI SphI BciVI
 | | | |
 18961 ggccggcgcgctgcaccgtcgcatgcgcggcggtatcctgccctccttattccactga 19020
 -----+-----+-----+-----+-----+-----+-----+-----+
 ccgccgcgcgagcgtggcagctacgcgcgccataggacggggaggaataaggtgact

 Bsp1286I
 BmgI
 BseSI
 HaeII
 SacII BsaHI
 MspAII NarI
 BstDSI BanI
 | | | |
 19021 tcgccgcggcgattggcgccgtgcccgaattgcacgtggtccttgaggcgagagac 19080
 -----+-----+-----+-----+-----+-----+-----+-----+
 agcgggcgccgctaaccggcgacgggccttaacgtaggcacgggaacgtccgcgtctctg

 NspI BspGI
 | |
 19081 actgattaaaaacaagttgcatgtggaaaaatcaaaataaaaagtctggactctcacgct 19140
 -----+-----+-----+-----+-----+-----+-----+-----+
 tgactaattttgttcaacgtacaccttttttagttttttttcagacctgagagtgcga

FIGURE 28



FIGURE 28

20461 acaacgaagac agacgagcaagctgagcagcaaaaaactcacgtat gcagg 20520
 tgttgcttctgcttcctcgtcgttcgactcgtctttttgagtgacataaacccgtcc

HaeII SspI
 20521 cgccttattctggtataaatattacaaaggagggtattcaaatagggtgcgaagggtcaaa 20580
 gcggaataagaccatatttataatgtttctccataagtttatccacagcttccagttt

Tth111II EcoNI
 20581 cacctaaatatgccgataaaacatttcaacctgaacctcaaataggagaatctcagtggt 20640
 gtggatttatacggctattttgtaaagttggacttggagtttatcctcttagagtcacca

VspI MspAII PvuII
 20641 acgaaactgaaattaatcatgcagctgggagagtccttaaaaagactaccccaatgaaac 20700
 tgctttgactttaattagtagctcgacctctcaggaattttctgatggggttactttg

NdeI RleAI BsmI
 20701 catgttacgggttcataatgcaaaacccacaaatgaaatggagggaaggcattcttgtaa 20760
 gtacaatgccaaagtatacgttttgggtgtttacttttacctccggttccgtaagaacatt

20761 agcaacaaaatggaaagctagaaagtcaagtggaaatgcaatttttctcaactactgagg 20820
 tcgttggttttacctttcgatctttcagttcacctttacgttaaaaagagttgatgactcc

BsiEI BsrDI BsrGI TatI
 20821 cgaccgcaggcaatggtgataacttgactcctaagtggtattgtacagtgaagatgtag 20880
 gctggcgctcgttaccactattgaactgaggatttcaccataacatgtcacttctacatc

NspI BssSI
 20881 atatagaaacccagacactcatattttcttacatgccactattaaggaaggtaactcac 20940
 tatactcttggggtctgtgagtataaagaatgtacgggtgataattccttccattgagtg

HaeI StuI BglI BsrDI
 20941 gagaactaatgggccaacaatctatgcccaacaggcctaattacattgcttttagggaca 21000
 ctcttgattaccggttggttagatacgggttggtccggttaattgtaacgaaaatccctgt

TaqII
 21001 attttattggtctaatgtattacaacagcacgggtaatatgggtgttctggcgggccaag 21060
 taaaataaccagattacataatgtgtcgtgcccattatacccacaagaccgcccgttc

Tth111II BsmI Tth111II
 21061 catcgagttgaatgctgtttagatttgcaagacagaaacacagagctttcataccagc 21120
 gttagcgtcaacttacgacaacatctaaacgttctgtctttgtgtctcgaaagtatggtcg

DrdII SexAI HincII
 21121 ttttgcttgattccattggtgatagaaccagggtacttttctatgtggaatcagggtgttg 21180
 aaaacgaactaaggttaaccactatcttgggtccatgaaaagatacaccttagtccgacaac

21181 acagctatgatccagatgttagaattattgaaaatcatggaactgaagatgaacttccaa 21240
 tgcgatactagggtctacaatcttaataacttttagtaccttgacttctacttgaaggtt

Eco57I BmrI VspI StyI
 21241 attactgctttccactgggaggtgtgattaatacagagactcttaccagggtaaaacctaa 21300
 taatgacgaaagggtgacctccacactaattatgtctctgagaatggttccattttggat

EcoNI SfcI ApoI MmeI
 21301 aaacagggtcaggaaaatggatgggaaaaagatgtacagaattttcagataaaaatgaaa 21360
 tttgtccagtccttttacctacctttttctacgatgtcttaaaagtctatttttacttt

FIGURE 28

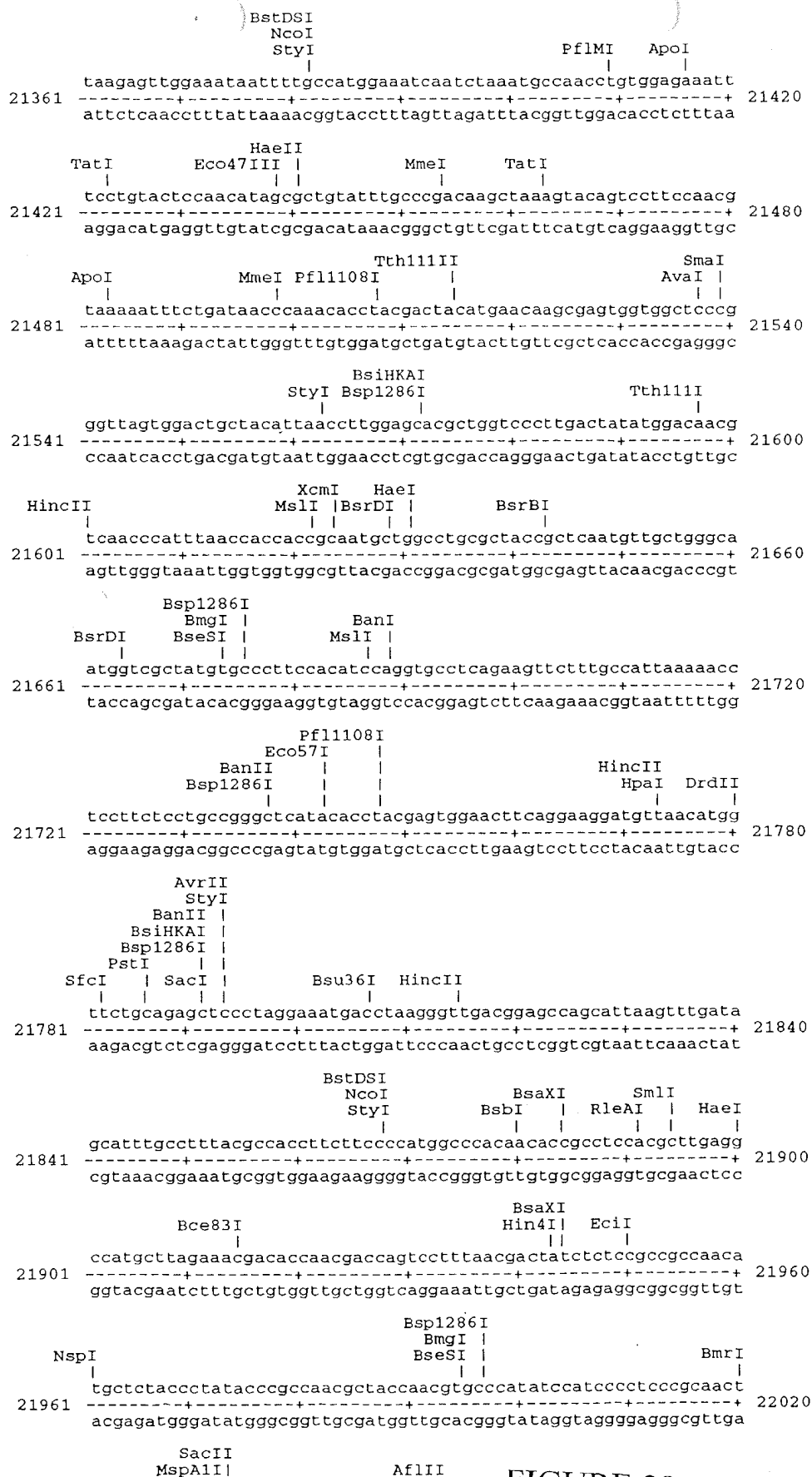


FIGURE 28

BstDSI | SmlI | HriI
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 cccgcgaaaggcgccgacccggaagtgcgcggaattctgattcctttgggtagtgacc
 Pfl1108I
 BanII |
 Bsp1286I |
 AvaI |
 22081 gctcgggctacgacccttattacacctactctggctctataccctacctagatggaacct 22140
 cgagcccgatgctgggaataatgtggatgagaccgagatatgggatggatctaccttgga
 HaeI MspAII
 MscI EarI | HaeI
 EaeI | DrdI | PvuII |
 22141 tttacctcaaccacacctttaagaagggtggccattacctttgactcttctgtcagctggc 22200
 aaatggagttggtgtggaattcttccaccggaatggaaactgagaagacagtcgaccg
 BsrDI HaeII
 Eco47III | HincII
 22201 ctggcaatgaccgctgttaccaccaacgagtttgaaattaagcgctcagttgacgggg 22260
 gaccgttactggcgacgaatgggggttgctcaaactttaattcgcgagtcaactgcccc
 AclI BmrI DrdII PflMI | NheI
 22261 aggggttacaaacgttgccagtgtaacatgaccaaagactggttctctggtacaaatgctag 22320
 tcccaatgttgcaacgggtcacattgtactgggttcttgaccaaggaccatgtttacgatc
 NspI
 TatI |
 22321 ctaactacaacattggctaccagggttcttatatcccagagagctacaaggaccgcatgt 22380
 gattgatgttgtaaccgatggtcccggaagatatagggtctctcgatgttctggcggtaca
 Bsp24I Bsp24I
 22381 actccttcttttagaaacttccagcccatgagccgtcaggtggtggatgataactaaatata 22440
 tgaggaagaaatctttgaaggtcgggtactcggcagtcaccacactactatgatttatgt
 PflMI BsbI
 22441 aggactaccaacaggtgggcatectacaccaacacaacactctggatttgggtgctacc 22500
 tcttgatggttgteccaccgtaggatgtggttgtgtgttgagacctaaacaaccgatgg
 HaeI
 StuI |
 22501 ttgccccaccatgcgcgaaggacagcctaccctgctaacttcccctatccgcttatag 22560
 aacgggggtggtacgcgcttctctgtcggatgggacgattgaaggggataggcgaatatc
 BsiEI
 PvuI
 SgfI BpmI
 22561 gcaagaccgcagttgacagcattaccagaaaaagtttctttgcatcgacccctttggc 22620
 cgttctggcgtcaactgtcgtaatgggtctttttcaaagaaacgctagcgtgggaaaccg
 BstDSI
 NcoI
 StyI
 22621 gcatcccatctccagtaactttatgtccatgggcgactcacagacctgggccaacc 22680
 cgtagggtaagaggtcattgaaatacaggtaccgcggtgagtgctggaccgggttttg
 BstDSI
 BamHI NcoI
 BstYI StyI
 22681 ttctctacgccaactccgcccacgcgctagacatgacttttgaggtggatcccatggacg 22740
 aagagatgcgggttgaggcgggtgcgcgatctgtactgaaaactccacctagggtacctgc
 BsiEI
 EaeI |
 EagI |

FIGURE 28

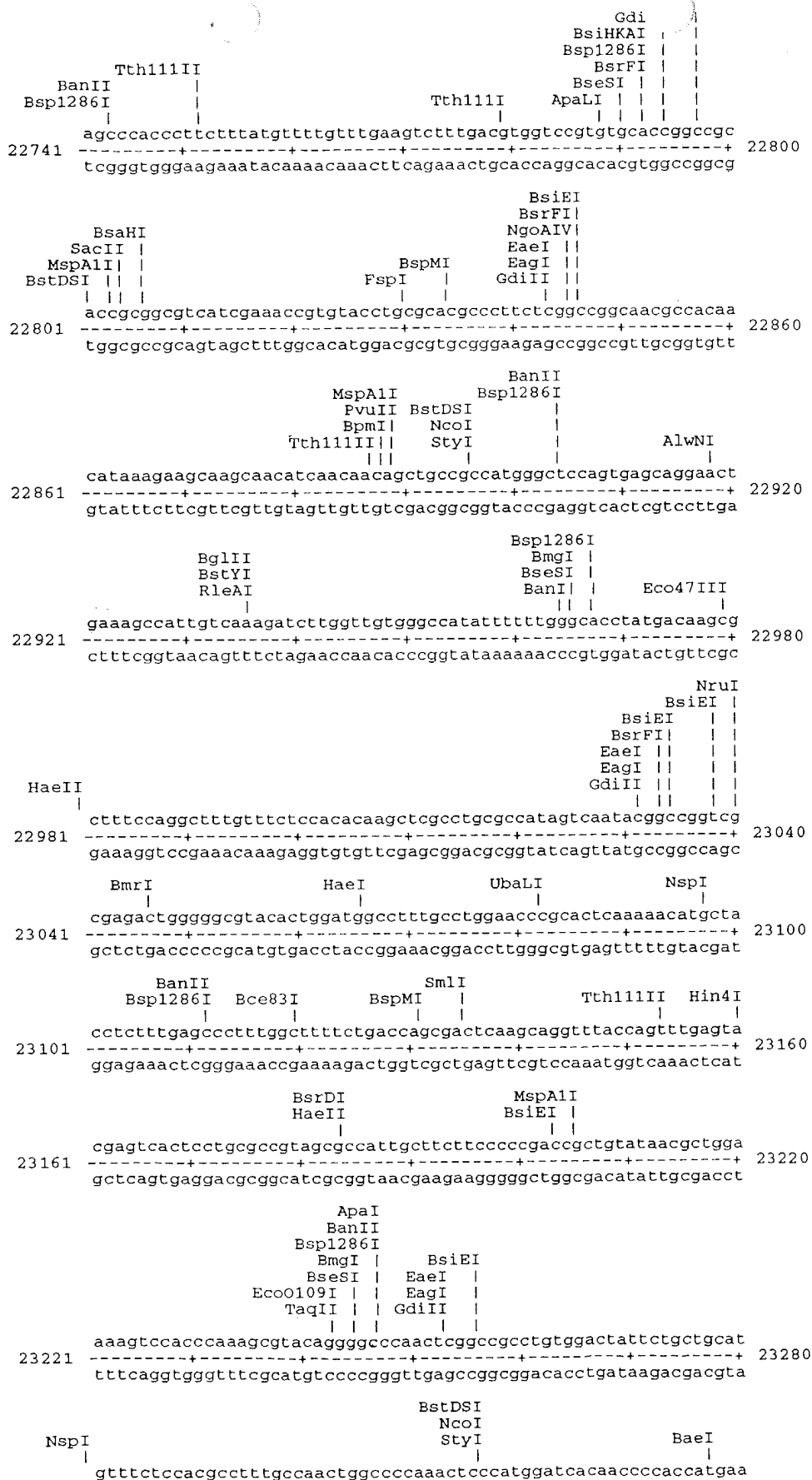


FIGURE 28

Bsp1286I
 BmgI |
 BseSI |
 HgiEII |
 BciVI |
 Hin4I | MslI | BplI | BstEII |
 24001 gttgcactcgccacgtagtggcatcaaaagggtgacccgtgcccggtctggcggttaggata 24060
 caacgtgagcgtggcatcacgtagtttccactggcacgggcccagaccgcaatcctat
 AlwNI | Bpu10I |
 HaeII | Eco57I |
 24061 cagcgccctgcataaaaagccttgatctgcttaaaagccacctgagcctttgcgccttcaga 24120
 gtgcgggacgtattttcggaaactagacgaattttcggtggactcggaacgcggaagtct
 MmeI
 BsiHKAII |
 Bsp1286II |
 BseSI | |
 NspI | BstAPI | EaeI | BglI | BglI | SfiI | ApaLI | | |
 24121 gaagaacatgccgcaagacttgccggaactgattggccggacagggcgctcggtgcac 24180
 cttcttgtagcggcgttctggaacggcctttgactaacggcctgtccggcgacgacgctg
 BglII | BsaWI |
 BstYI | BsrFI |
 BsgI | BsbI | PinAI |
 24181 gcagcaccttgctcggtgttgagatctgcaccacatttcggccccacgggttcttcac 24240
 cgctcggtggaacgcagccacaacctctagacgtggtgtaaagccggggtggccaagaagtg
 Eco57I | BssHII |
 HaeI | BssHII | |
 24241 gatcttggccttgctagactgctccttcagcgcgctgcccggttttcgctcgtcacatc 24300
 ctagaaccggaacgatctgacgaggaagtgcgcgcgcgacgggcaaaagcgagcagtgtag
 BsiHKAII |
 Bsp1286I |
 BsaAI | |
 PmlI | |
 AflII |
 AccI | SmlI |
 24301 catttcaatcacgtgctccttatttatcataatgcttcggtgtagacacttaagctcgcc 24360
 gtaaagttagtgacagaggaataaatagtattacgaaggcacatctgtgaattcgagcgg
 BanII |
 Bsp1286I |
 BssSI |
 Tth111II | |
 BsgI | | |
 BstDSI | | |
 MspAII |
 24361 ttcgatctcagcgcagcgggtgcagccacaacgcgcagcccggtgggctcggtgatgcttcta 24420
 aagctagagtcgctgcgcacgtcggtgttgccgctcgggcacccgagcactacgaacat
 PstI |
 SbfI |
 BstEII | BspMI | SfcI | | SfcI | |
 24421 gggtcacctctgcaaacgactgcaggtacgcctgcaggaatcgcccatcatcggtcacaaa 24480
 ccagtgagagcgtttgctgacgtccatgcggacgtccttagcggggtagtagcagtggtt
 BsiHKAII |
 Bsp1286I |
 SacII |
 MspAII | |
 MspAII | BstDSI | |
 PvuII | BseRI | | |
 24481 ggtcttgttgctggtgaagggtcagctgcaaccgcggtgctcctcgcttcagccaggtctt 24540
 ccagaacaacgaccacttcagtcgacgttgggcccacgaggagcaagtcggtccagaa
 BsiEI |
 EaeI | |
 EagI | |
 GdiII | |
 24541 gcatacggccgcccagagcttccacttggtcaggcagtagtttgaagttcgccctttagatc 24600
 cgtatgccggcggtctcgaagggtgaaccagtcgctcatcaaaacttcaagcggaatctag

BssHII

FIGURE 28

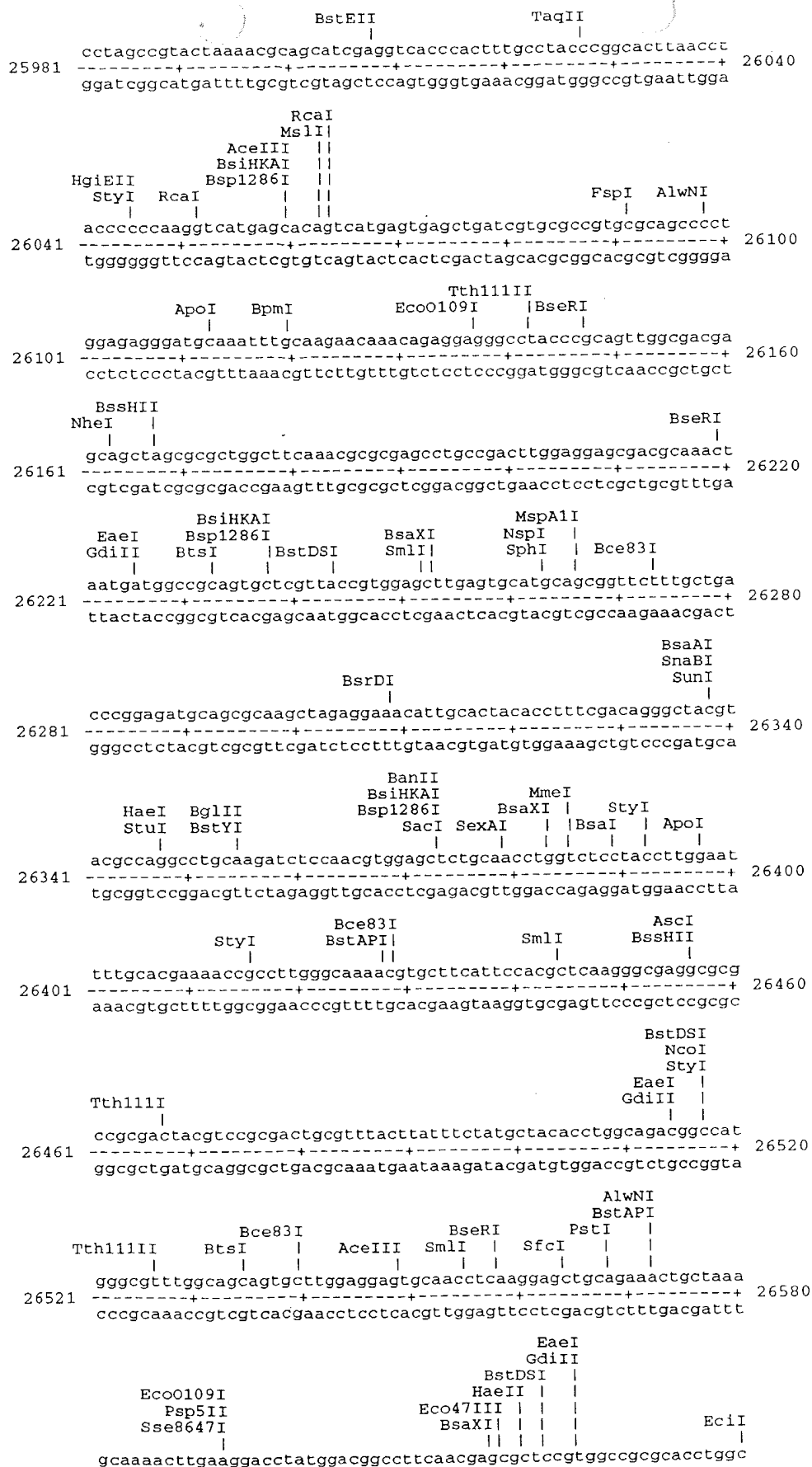


FIGURE 28

26581 -----+-----+-----+-----+-----+ 26640
 cgttttgaacttctggatacctgccggaagtgtctcgcgaggcaccggcgctggaccg
 EcoNI AlwNI
 26641 -----+-----+-----+-----+-----+ 26700
 ggacatcattttccccgaacgctgttaaaacccctgcaacagggtctgccagacttcac
 cctgtagtaaaaggggcttgcggacgaattttgggacgttgtcccagacggtctgaagtg
 Bpu10I
 HaeII
 NspI Eco47III
 26701 -----+-----+-----+-----+-----+ 26760
 cagtcaaagcatgttgcagaacttttaggaactttatcctagagcgctcaggaatcttgcc
 gtcagtttctgtacaacgtcttgaaatccttgaaataggatctcgcgagtccttagaacgg
 BsiHKA I
 Bsp1286I
 BseSI
 BspMI
 AarI ApaLI
 Bsp1286I
 BmgI
 BseSI
 EciI
 BsmI
 26761 -----+-----+-----+-----+-----+ 26820
 cgccacctgctgtgcacttccttagcgactttgtgcccattaagtaccgcgaatgcctcc
 gcggtggacgacacgtgaaggatcgctgaaacacgggtaattcatggcgcttacgggagg
 NheI
 PstI
 BtsI SfcI
 26821 -----+-----+-----+-----+-----+ 26880
 gccgctttggggccactgctaccttctgcagctagccaactaccttgccctaccactctga
 cggcgaaaccccggtgacgatggaagacgtcgatcggttgatggaacggatggtgagact
 BsrBI
 BbsI
 AccI
 BstAPI
 BpmI
 26881 -----+-----+-----+-----+-----+ 26940
 cataatggaagacgtgagcggtgacggtctactggagtgtcactgtcgctgcaacctatg
 gtattaccttctgcactcgccactgccagatgacctcacagtgcagcgacgttggtgatac
 BsrBI
 MspAII
 PvuII
 AceIII
 BanI
 26941 -----+-----+-----+-----+-----+ 27000
 caccgcgcacgctccctgggtttgcaattcgagctgcttaacgaaagtcaaattatcgg
 gtggggcggtggcgagggaacaaacggttaagcgtcgacgaattgcttctcagtttaatagcc
 SacII
 MspAII
 BstDSI
 AhdI
 HaeIV
 Hin4I
 KpnI SfcI
 27001 -----+-----+-----+-----+-----+ 27060
 tacctttgagctgcaggggtccctcgctgacgaaaagtcgagggtccggggttgaaact
 atggaaactcgacgtcccaggagcgactgctttcaggcgcgaggccccaactttga
 AatII
 BsaHI
 ApoI
 Bsu36I
 27061 -----+-----+-----+-----+-----+ 27120
 cactccggggctgtggacgtcggttaccttcgcaattttgtacctgaggactaccacgc
 gtgaggccccgcacactgcagccgaatggaagcgtttaaacatggactcctgatggtgcg
 Pfl1108I
 BssSI UbaLI
 BbsI
 27121 -----+-----+-----+-----+-----+ 27180
 ccacgagattaggttctacgaagaccaatccccgccgccaatgctggagcttaccgcctg
 ggtgctctaatacaagatgcttctggttagggcgggcggtttacgcctcgaatggcgag
 MunI
 HaeI
 MscI
 EaeI
 BstXI
 27181 -----+-----+-----+-----+-----+ 27240
 cgtcattaccaggggccacattcttggccaattgcaagccatcaacaaagcccgccaaga
 gcagtaatgggtcccggtgtaagaaccggttaacggttcggtagtgtttcgggcggttct
 BmrI
 AhdI
 HaeIV
 Hin4I
 Pfl1108I
 BanII
 BsiHKA I
 Bsp1286I
 SacI
 gtttctgctacgaaaggacggggggttacttggacccccagtcggcgaggagctcaa

FIGURE 28

[illegible]

FIGURE 28

SfcI BsgI BsrFI SgrAI MspAII
 27841 cccgtaacatcctgcattactaccgtcatctctacagccatactgcacggcgccagcg 27900
 gggcattgtaggacgtaatgatggcagtagagatgtcgggtatgacgtggccgcccgtcgc
 EaeI GdiIII BsiEI BsaWI
 MspAII MspAII MspAII
 27901 gcagcggcagcaacagcagcggccacacagaagcaaggcgaccggatagcaagactctg 27960
 cgtcgccgctcgttgtcgtcgccgggtgtgtcttcgtttccgctggcctatcgttctgagac
 BsaHI NarI BanI BseRI
 BseRI HaeII Eco47III
 27961 acaaagcccaagaaatccacagcggcgccagcagcaggaggagcgctcgtctggtg 28020
 tgtttcgggttcttttaggtgtcgccgcccgtcgtcgtcctcctcctcgacgcagaccgc
 HaeII
 28021 cccaacgaaccggtatcgaccgcgagcttagaaacaggatttttccactctgtatgct 28080
 gggttgcttgggcatagctgggcgctcgaatctttgtcctaaaaagggtgagacatacga
 AceIII BsaI
 28081 atatttcaacagagcaggggccaagaacaagagctgaaaataaaaaacaggctctctgcga 28140
 tataaagttgtctcgtcccggttcttgttctcgacttttatttttgtccagagacgct
 MspAII PvuII Eco57I
 28141 tccctcaccgcgagctgcctgtatcacaaaagcgaagatcagcttcggcgccagctggaa 28200
 agggagtgggcgctcgacggacatagtggttttcgcttctagtcgaagccgctgcgacctt
 BbsI EarI BssHII AflII SmlI SpeI
 28201 gacgcggaggctctcttcagtaatactgcgcgctgactcttaaggactagtttcgcgcc 28260
 ctgcgcctccgagagaagtcatttatgacgcgcgactgagaattcctgatcaaacgcggtg
 HaeII BsaHI NarI BanI
 EaeI GdiIII Bsp24I
 ApoI BpmI BsaXI MspAII
 28261 ctttctcaaatttaagcgcgaaaactacgtcatctccagcggccacacccggcgccagca 28320
 gaaagagtttaaatcgcgcttttgatgcagtagaggtcgccggtgtgggcccgcggtcgt
 Bsp24I AflIII NspI
 AlwNI HaeII ApoI BspLU11I
 28321 cctgtcgtcagcgccattatgagcaaggaaattccacgcgcctacatgtggagtaccag 28380
 ggacagcagtcgcggtaatactcgttcccttaagggtgcgggatgtacacctcaatggtc
 AceIII BpmI
 28381 ccacaaatggacttgcggctggagctgcccagactactcaaccgaataaaactacatg 28440
 ggtgtttaccctgaacgcgcgacctcgacgggttctgatgagttgggcttatttgatgtac
 HincII RleAI
 Eco0109I SmaI
 Psp5II AvaI
 SanDI EcoRV
 ApoI EcoRI
 28441 agcgcgggacccacatgatatccgggtcaacggaatccgcgcccaccgaaaccgaatt 28500
 tcgcgcctcgggtgtactatagggccagttgccttaggcgcggtggctttggcttaa
 28501 ctcttggaaacaggcggtattaccaccacacctcgtaataaccttaaccccgtagttgg 28560

FIGURE 28

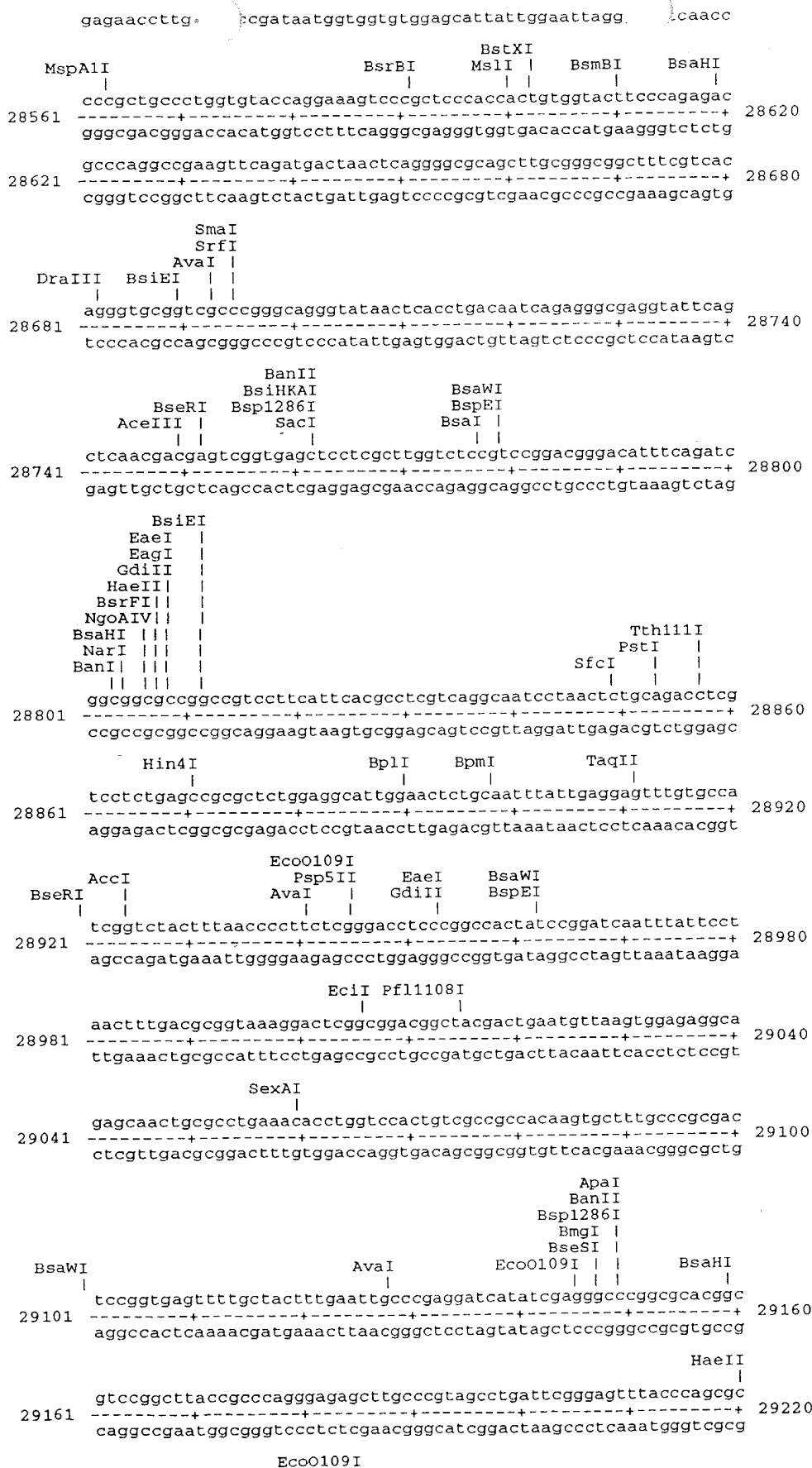


FIGURE 28

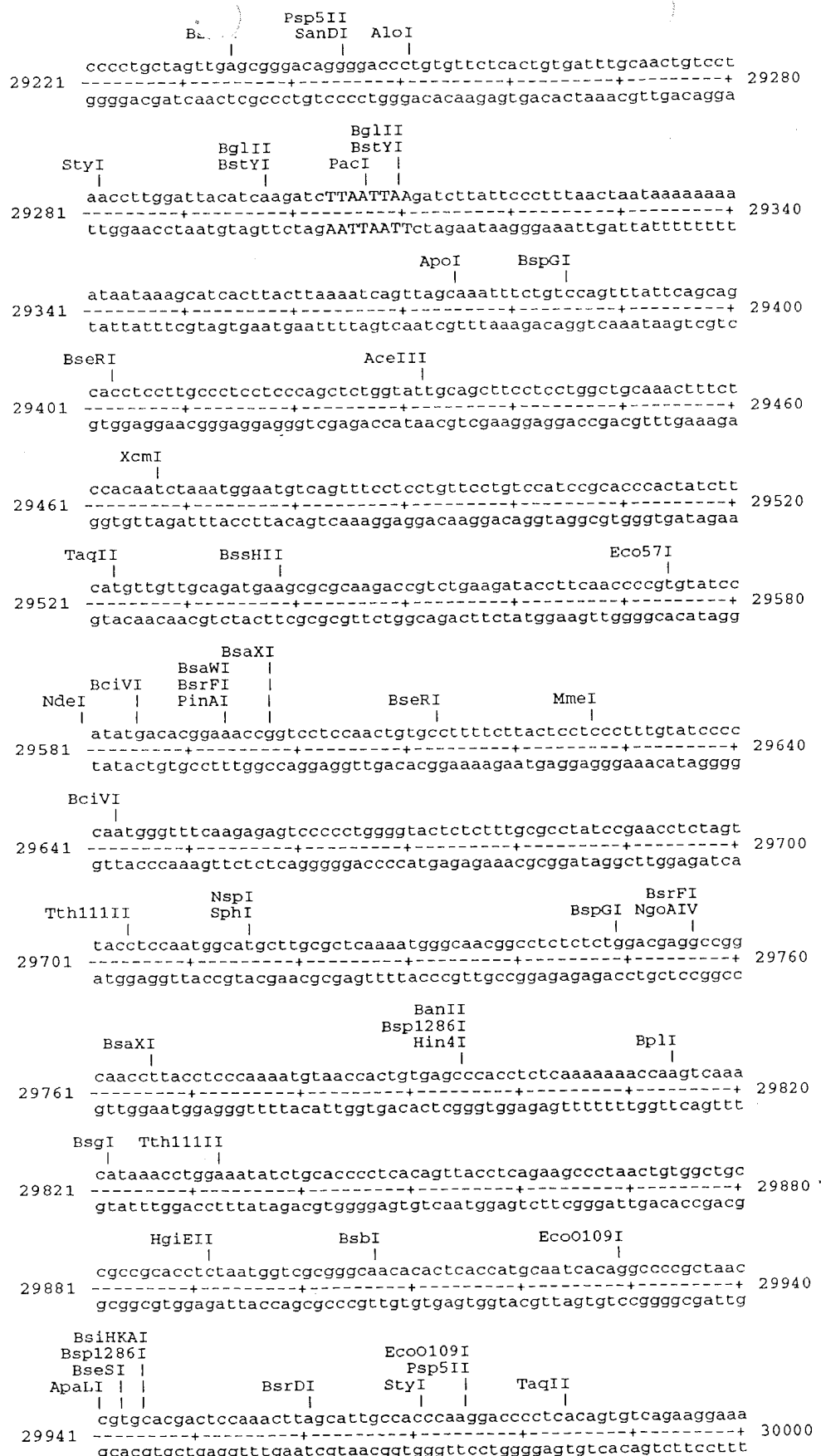


FIGURE 28

30001 gctagccctgcaaacatcaggccccctcaccaccaccgatagcagtagcccttactatcac 30060
 cgatcgggacgtttgtagtcgggggagtggtggtggtatcgatcatgggaatgatagtg
 30061 tgcctcaccctcctaactactgccactggtagcttgggcattgacttgaaagagcccat 30120
 acgggagtggggagattgatgacggtgaccatcgaaccgtaactgaactttctcgggta
 30121 ttatacacaaaatggaaaactaggactaaagtacggggctcctttgcatgtaacagacga 30180
 aatattgtgtttaccttttgatcctgatttcacgccccgaggaacgtacattgtctgct
 30181 cctaaacactttgaccgtagcaactgggtccagggtgactattaataacttccttgca 30240
 ggatttgtgaaactggcatcgttgaccagggtccacactgataattattatgaaggacgt
 30241 aactaaagttactggagccttgggttttgattcacaaggcaatatgcaacttaattgtagc 30300
 ttgatttcaatgacctcgggaacccaaaactaagtgttccgttatacgttgaattacatcg
 30301 aggaggactaaggattgattctcacaacagacgccttatacttgatgttagttatccggt 30360
 tctcctgattcctaactaagagttttgtctcggaatatgaactacaatcaataggcaa
 30361 tgatgctcaaaaccaactaaatctaagactaggacagggccctctttttataaactcagc 30420
 actacgagttttggttgatttagattctgacgtgccccgggagaaaaatatttgagtcg
 30421 ccacaacttggaatattaactacaacaaaggcctttacttggtttacagcttcaacaattc 30480
 ggtggtgaacctataattgatgtgttttcggaaatgaacaaatgtcgaagtttgtaag
 30481 caaaaagcttgaggttaacctaaagcaactgccaaggggttgatgtttgacgctacagccat 30540
 gtttttcgaactccaattggattcgtgacggttccccaaactacaaactgcgatgtcggta
 30541 agccattaatgcaggagatgggcttgaatttggttcacctaatagcacaaacacaaatcc 30600
 tcggtaattacgtctctacccgaacttaaccaagtggattacgtggtttgtgttagg
 30601 cctcaaaacaaaaattggccatggcctagatttgattcaaaacaggctatggttcctaa 30660
 ggagttttgttttaaccgggtaccggatcttaaaactaagtttgttccgataccaaggatt
 30661 actaggaactggccttagttttgacagcacaggtgccattacagtaggaacaaaaataa 30720
 tgatccttgaccggaatcaaaactgtcgtgtgcacggtaatgtcatcctttgttttatt

Restriction sites (Enzymes) indicated above the sequence:
 30001: NheI, Tth111II, BclI
 30061: XcmI, BanII, Bsp1286I
 30121: BanII, Bsp1286I, NspI
 30181: BspGI, VspI
 30241: StyI, BpmI
 30301: Hin4I, BsaHI
 30361: ApaI, BanII, Bsp1286I, BmgI, BseSI, EcoO109I, EcoO109I
 30421: PflMI, RleAI, HaeI, StuI
 30481: SmlI, Bpu10I, Tth111II, StyI, Bce83I, BtsI, SfcI, HindIII, HincII, HpaI
 30541: VspI, ApoI, DrdII
 30601: Tth111II, EaeI, HaeI, ApoI, Tth111II, DrdII, EcoNI
 30661: HaeI, BanI

FIGURE 28

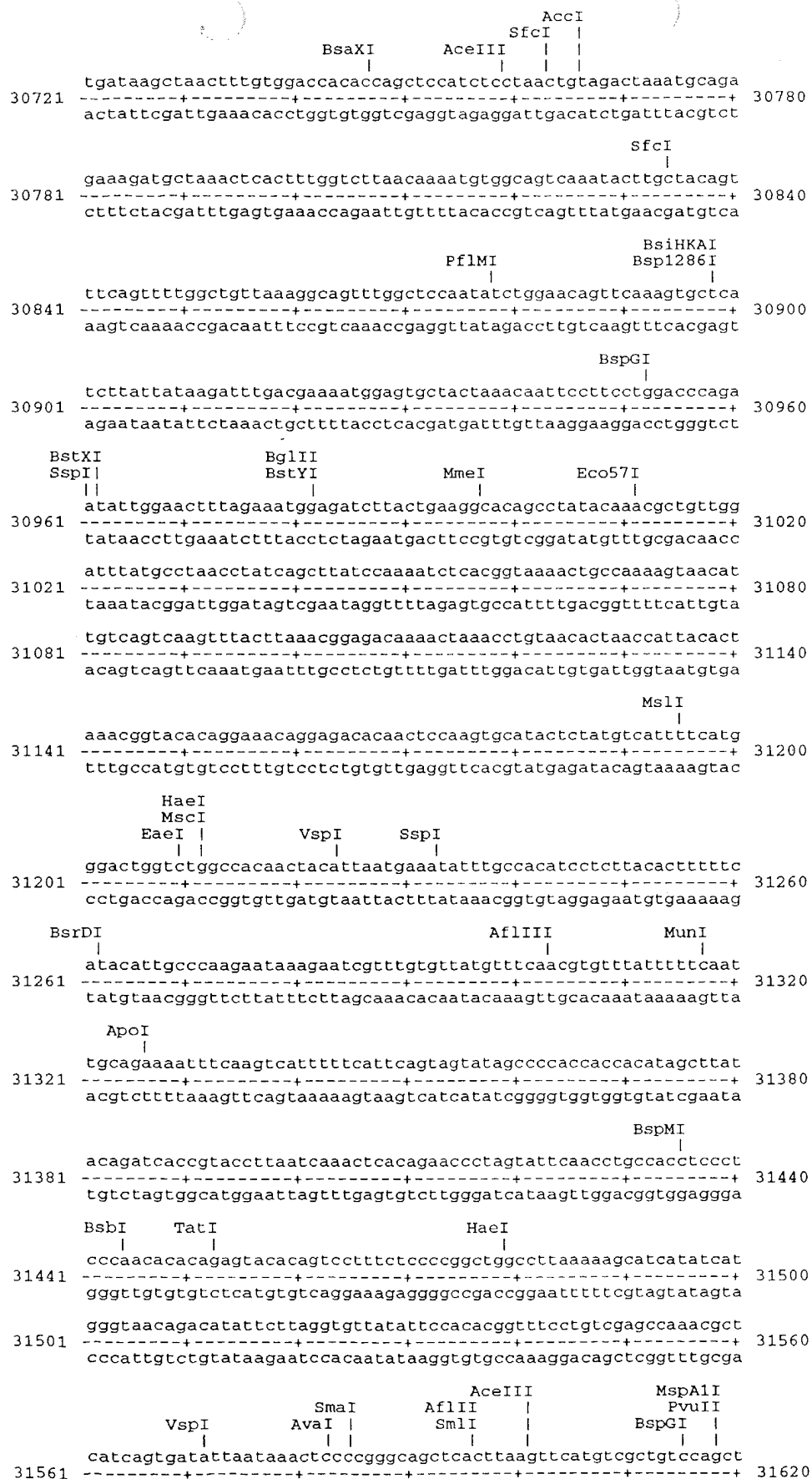


FIGURE 28

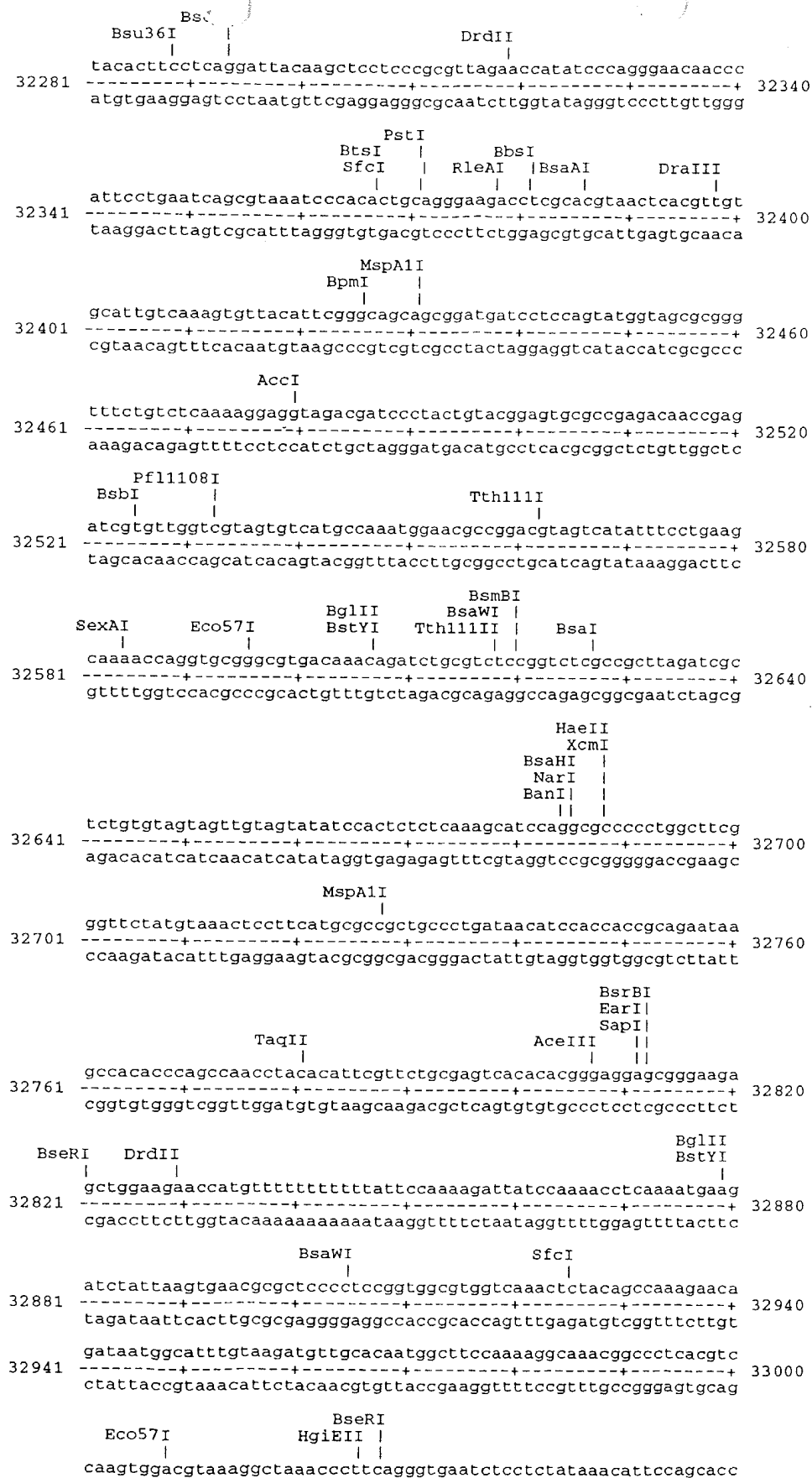


FIGURE 28

33001 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33060
gttcacctgca cccgatttgggaagtcccacttagaggagatatttctaaggtcgcgg
33061 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33120
ttcaaccatgccccaaataattctcatctcgccaccttctcaatatatctctaagcaaatc
aagttggtacgggtttattaagagtagagcgggtggaagagttatatagagattcgttttag

BpmI
EaeI |
SspI GdiII | Eco57I Bce83I | SmlI
33121 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33180
ccgaatattaagtccggccatttgtaaaaatctgctccagagcgcctccaccttcagcct
ggcttataattcaggccggtaacatttttagacgaggtctcgcgagggtggaagtcgga

Tth111II
RcaI | ApoI |
33181 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33240
caagcagcgaatcatgattgcaaaaattcaggttcctcacagacctgtataagattcaaa
gttcgtcgcttagtactaacgtttttaagccaaggagtgctcgacatattctaagttt

EcoO109I MspAII BsgI
Psp5II PvuII BspMI
33241 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33300
agcggaaacattaacaaaaataccgcgcatcccgtaggtcccttcgcagggccagctgaaca
tcgccttgtaattgtttttatggcgctagggcatccagggaagcgtcccggtcgacttgt

EaeI
GdiII |
MslI BsgI |
33301 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33360
taatcgtgcaggtctgcacggaccagcgccggaacttccccgcaggaaccttgacaaaa
attagcacgtccagacgtgcctggcgccggtgaaggggagggtccttggaactgtttt

RleAI
33361 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33420
gaaccacactgattatgacacgcatactcggagctatgctaaccagcgtagccccgatg
cttgggtgtgactaataactgtgcgtatgagcctcgatacgattggtcgcatcggggtac

HindIII
33421 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33480
taagctttgttgcatgggcgccgatataaaatgcaaggtgctgctcaaaaaatcaggcaa
attcgaaacaacgtacccgccgtatattttacgttcacgacgagtttttagtcggtt

Pfl1108I MslI BspMI
33481 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33540
agcctcgcgcaaaaaaagaaagcacatcgtagtcatgctcatgcagataaaggcaggttaag
tcggagcgcggttttttcttctgtagcatcagtagttagctattttccgtccattc

BsaWI NspI
BspEI DrdII AflIII BspLUIII Tth111II
33541 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33600
ctccggaaccaccacagaaaaagacaccatttttctctcaaacatgtctcggggtttctg
gaggccttggtggtgtctttttctggtgtaaaaagagagtttgtagacagcgccaaagac

DraI
33601 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33660
cataaacacaaaaataaaataacaaaaaacatttaaaccattagaagcctgtcttacaaca
gtatttggtgttttattttattgtttttttgtaaatttgtaattcttcggacagaaatgttgt

BglI
EaeI BsrFI |
GdiII NgoAIV |
33661 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33720
ggaaaaacaacccttataagcataagacggactacggccatgcccgtgaccgtaaaaa
cctttttgttggaatatctgtattctgctgatgccggtacggccgactggcattttt

BstEII TaqII BsaWI
BseRI Hin4I AceIII BspEI
33721 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33780
aactgggtcaccgtgattaaaaagcaccgacagctcctcggtcatgtccggagtcata
ttgaccagtggcactaatttttctggtggtgctgtaggagccagtagcaggtcagtat

TaqII BsiEI
33781 -----+-----+-----+-----+-----+-----+-----+-----+-----+-----+ 33840
atgtaagactcggtaaacacatcaggttgattcatcggtcagtgctaaaaagcgacgaa
tacattctgagccatttctgtagtccaactaagtagccagtcacgatttttctgctggtt

FIGURE 28


```

      TaqII
      SmaI
      Aval
      |
      |
      |
33841  atagcccggggaatacataccgcaggcgtagagacaacattacagcccccataggagg 33900
      -----+-----+-----+-----+-----+
      tatcggggccccccttatgtatgggcgtccgcacatctctgttgtaatgtcgggggtatcctcc

      VspI
      |
      |
      |
33901  tataacaaaattaataggagagaaaaaacataaaacacctgaaaaacccctcctgcctagg 33960
      -----+-----+-----+-----+-----+
      atattgttttaattatcctctctttttgtgtatttggacttttgggaggacggatcc

      HaeII
      |
      |
      |
      BpmI      BsrBI      Eco47III      MspAII
      |         |         |         |
33961  caaaatagcacccctcccgctccagaacaacatacagcgcttcacagcggcagcctaacag 34020
      -----+-----+-----+-----+-----+
      gttttatcgtgggagggcgagggtcttgtgtatgtcgcgaagtgtcgccgtcggattgtc

      BanI
      |
      |
      |
34021  tcagccttaccagtaaaaaagaaaacctattaaaaaacaccactcgacacggcaccagc 34080
      -----+-----+-----+-----+-----+
      agtcggaattgggtcatTTTTTCTTTTGGGATAATTTTTTGTGGTGAGCTGTGCGGTGGTCTG

      AceIII
      |
      |
      |
      BsgI
      |
34081  tcaatcagtcacagtgtaaaaaagggccaagtgcagagcgagtatatataggactaaaaa 34140
      -----+-----+-----+-----+-----+
      agttagtcagtggtcacatttttcccggttcacgtctcgctcatatatatcctgattttt

      TaqII
      |
      |
      |
34141  atgacgtaacgggttaaagtcacaaaaaacaccagaaaaccgcacgcaacctacgcc 34200
      -----+-----+-----+-----+-----+
      tactgcattgccaatttcaggtgtttttgtgggtcttttggcgtgcgcttggtatgcggg

      RleAI
      |
      |
      |
34201  agaaacgaaagccaaaaaacccacaacttctcctcaaatcgtcacttccggttttccacgtt 34260
      -----+-----+-----+-----+-----+
      tctttgctttcgggttttttgggtgttgaaggagtttagcagtgaaaggcaaaagggtgcaa

      BsaAI
      |
      |
      |
      SnaBI
      |
      |
      |
      BsbI
      |
      |
      |
      EciI
      |
34261  acgtaacttcccattttaagaaaactacaattcccaacacatacaagttactccgccta 34320
      -----+-----+-----+-----+-----+
      tgcattgaagggttaaaattcttttgatgttaagggttgtgtatgttcaatgaggcgggat

      aaacctacgtcacccgccccgttcccacgccccgcgcacgtcacaaactccacccctc
34321  -----+-----+-----+-----+-----+
      tttggatgcagtgggcggggcaagggtgcggggcgcggtgcagtgtttgaggtgggggag

      attatcatattggcttcaatccaaaataagggtatattattgatgatg
34381  -----+-----+-----+-----+-----+ 34427
      taatagtataaccgaagttaggttttattccatataataactactac

```

Enzymes that do cut:

AarI	AatII	AccI	AceIII	AcII	AflII	AflIII	AhdI
AloI	AlwNI	ApaI	ApalI	ApoI	AscI	AvaI	AvrII
BaeI	BamHI	BanI	BanII	BbsI	BbvCI	Bce83I	BcgI
BciVI	BclI	BglI	BglII	BmgI	BmrI	BplI	BpmI
Bpu10I	Bpu102I	BsaI	BsaAI	BsaBI	BsaHI	BsaWI	BsaXI
BsbI	BseRI	BseSI	BsgI	BsiEI	BsiHKA1	BsmI	BsmBI
Bsp24I	Bsp1286I	BspEI	BspGI	BspLU11I	BspMI	BsrBI	BsrDI
BsrFI	BsrGI	BssHII	BssSI	BstAPI	BstDSI	BstEII	BstXI
BstYI	BstZ17I	Bsu36I	BtsI	ClaI	DraI	DraIII	DrDI
DrdII	EaeI	EagI	EaRI	EciI	Eco47III	Eco57I	EcoNI
EcoO109I	EcoRI	EcoRV	FseI	FspI	GdiII	HaeI	HaeII
HaeIV	HgiEII	Hin4I	HincII	HindIII	HpaI	KpnI	MluI
MmeI	MscI	MslI	MspAII	MunI	NarI	NcoI	NdeI
NgoAIV	NheI	NotI	NruI	NsiI	NspI	PacI	Pfl1108I
PflMI	PinAI	PmeI	PmlI	PshAI	Psp5II	PstI	PvuI
PvuII	RcaI	RleAI	RsrII	SacI	SacII	SalI	SanDI
SapI	SbfI	ScaI	SexAI	SfcI	SfiI	SgfI	SgrAI
SmaI	SmlI	SnaBI	SpeI	SphI	SrfI	Sse8647I	SspI
StuI	StyI	SunI	SwaI	TaqII	TatI	Tth111I	Tth111II
UbaLI	VspI	XbaI	XcmI	XhoI	XmnI		

Enzymes that do not cut:

NspV

FIGURE 28

33001 -----+-----+-----+-----+-----+-----+ 33060
 gttcacctgca cccgatttgggaagtcccaacttagaggagatatattgtaaggctcgagg
 33061 -----+-----+-----+-----+-----+-----+ 33120
 ttcaacctatgccaaataattctcatctcgccaccttctcaatatatctctaagcaaatc
 aagttggtaggggtttattaagagtagagcggtggaagagttatatagagattcgttttag

BpmI
 SspI EaeI GdiII Eco57I Bce83I HaeII SmlI
 33121 -----+-----+-----+-----+-----+-----+ 33180
 ccgaatattaagtcggccattgttaaaaatctgctccagagcgccctccaccttcagcct
 ggcttataattcaggccggtaacatttttagacgaggtctcgcgagggtggaagtccga

Tth111II
 RcaI ApoI
 33181 -----+-----+-----+-----+-----+-----+ 33240
 caagcagcgaatcatgattgcaaaaattcaggttcctcacagacctgtataagattcaaa
 gttcgtcgcttagtactaacgtttttaagtccaaggagtgtctggacatatcttaagttt

EcoO109I MspAII BsgI
 Psp5II PvulII BspMI
 33241 -----+-----+-----+-----+-----+-----+ 33300
 agcggaaacattaacaaaaataccgcgatcccgtaggtcccttcgcagggccagctgaaca
 tcgccttgtaattgtttttatggcgctaggcatccagggaagcgctcccggtcgacttgt

EaeI
 GdiII
 MslI BsgI
 33301 -----+-----+-----+-----+-----+-----+ 33360
 taatcgtgcaggtctgcacggaccagcgcgcccaacttccccgccaggaaccttgacaaaa
 attagcacgtccagacgtgcctggtcgcgccggtgaagggcggtccttggaactgtttt

RleAI
 33361 -----+-----+-----+-----+-----+-----+ 33420
 gaaccacactgattatgacacgcatactcggagctatgctaaccagcgtagccccgatg
 cttgggtgtgactaataactgtgcgtatgagcctcgatacagattggtcgcatcggggtac

HindIII
 33421 -----+-----+-----+-----+-----+-----+ 33480
 taagctttgttgcattggcgccgatataaaatgcaaggtgctgctcaaaaaatcaggcaa
 attcgaacaaacgtacccgcgctatatatttaccgttcacgagagtttttttagtccgtt

Pfl1108I MslI BspMI
 33481 -----+-----+-----+-----+-----+-----+ 33540
 agcctcgcgcaaaaaaagaagacacatcgtagtcatgctcatgcagataaaggcaggttaag
 tcggagcgcggtttttttcttctgtgtagcatcagtagtacgtctatttccgtccattc

BsaWI NspI
 BspEI DrdII AflIII BspLUII Tth111II
 33541 -----+-----+-----+-----+-----+-----+ 33600
 ctccggaaccaccacagaaaaagacaccatttttctctcaaacatgtctcggggtttctg
 gaggccttggtggtgtctttttctgtggttaaaaagagagtttgtagacagcggccaaagac

DraI
 33601 -----+-----+-----+-----+-----+-----+ 33660
 cataaacacaaaaataaaataacaaaaaacatttaaacattagaagcctgtcttacaaca
 gtatttgtgttttattttattgttttttgtaaatttgtaattcttcggacagaatgttgt

BglI
 EaeI BsrFI
 GdiII NgoAIV
 33661 -----+-----+-----+-----+-----+-----+ 33720
 ggaaaaaacaaccttataagcataagacggactacggccatgcccggcgtgaccgtaaaaa
 cctttttgttggaatatctgtattctgctgatgcccgtacggccgactggcattttt

BstEII TaqII BseRI Hin4I AceIII BsaWI BspEI
 33721 -----+-----+-----+-----+-----+-----+ 33780
 aactgggtcacggtgattaaaaagcaccacgcagctcctcggtcatgtccggagtcata
 ttgaccagtgggcactaatttttctggtggtggtgtcgaggagccagtagcaggtcctcagtat

TaqII BsiEI
 33781 -----+-----+-----+-----+-----+-----+ 33840
 atgtaagactcggtaaacacatcaggttgattcatcggtcagtgctaaaaagcgaccgaa
 tacattctgagccatttgtgtagtccaactaagtagccagtcacgatttttctgctggctt

FIGURE 28